

FIG. 1

HPP-CFC (Colony #)

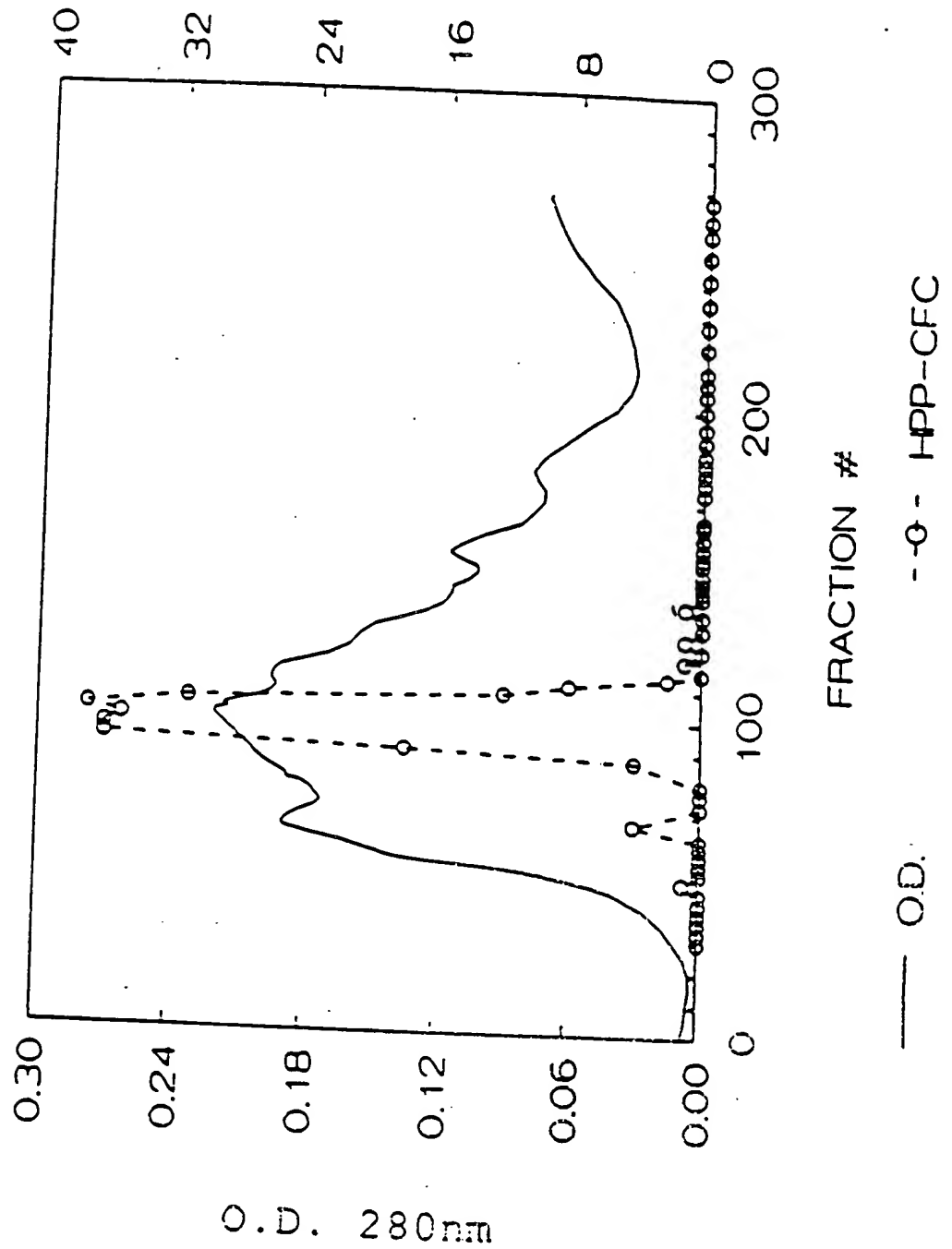


FIG. 2

HPP-CFC (Colony #)

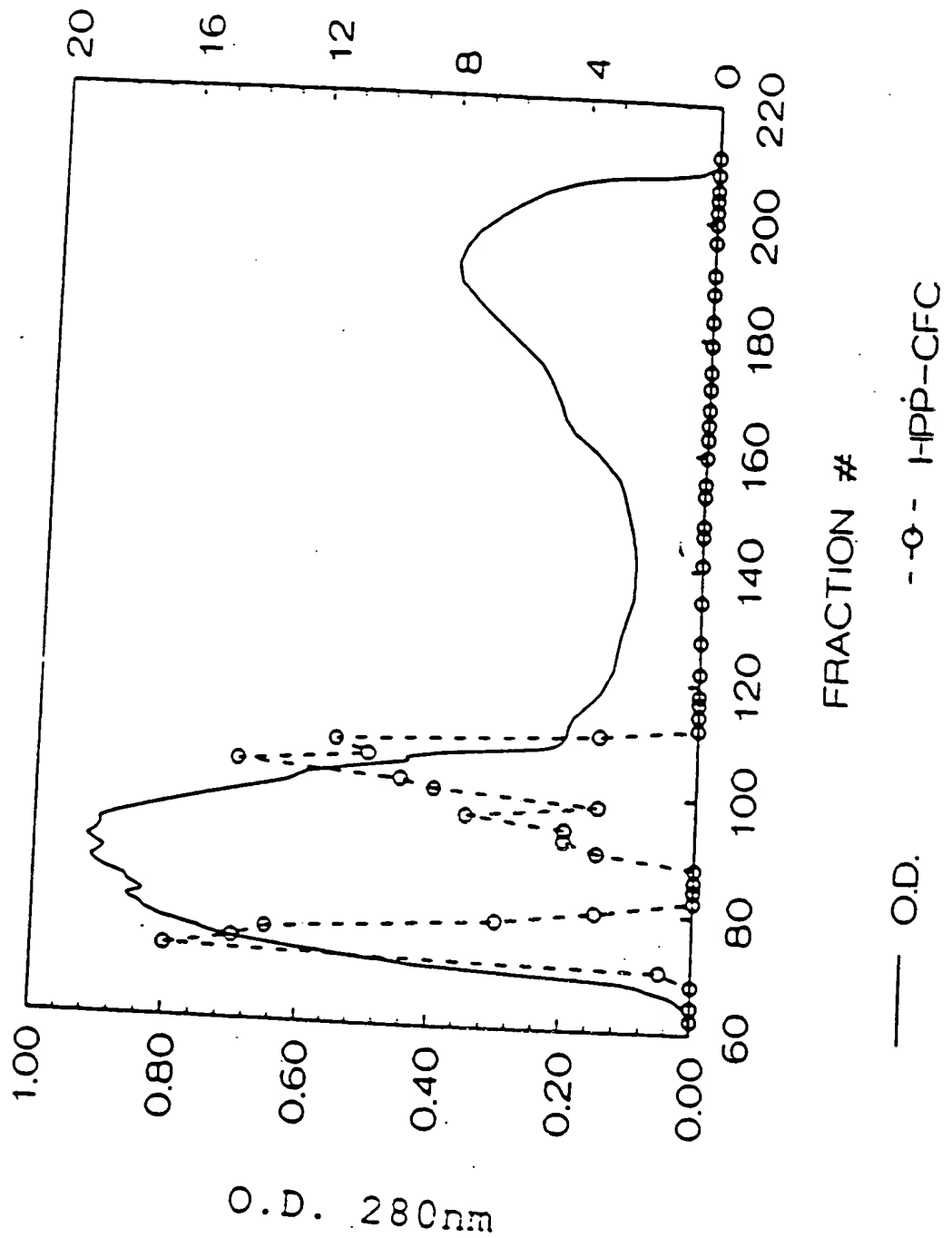


FIG.3

MC/9 CPM (X 10⁻³) OR HPP-CFC (col. #)

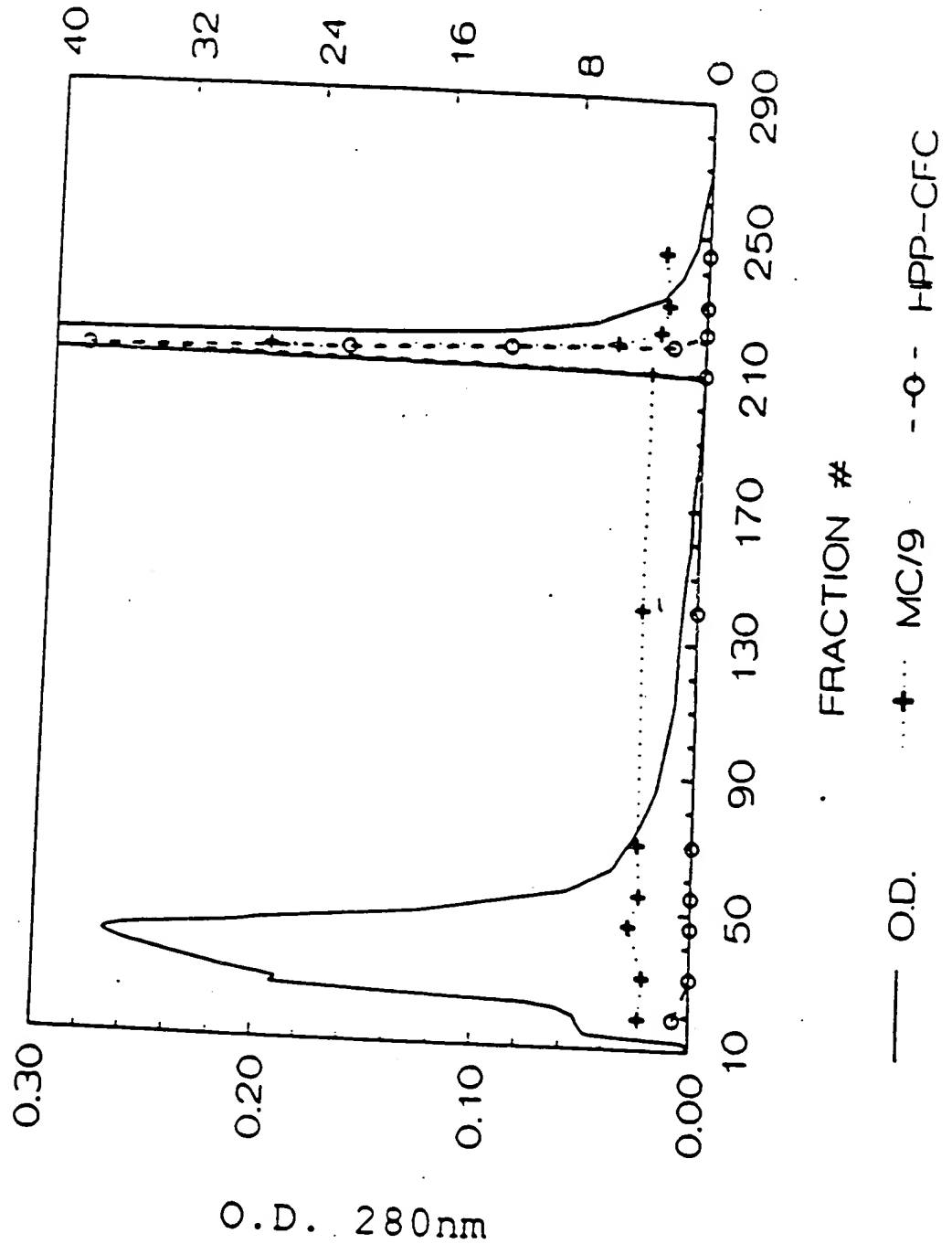


FIG. 4

MC/9 CPM ($\times 10^{-3}$)

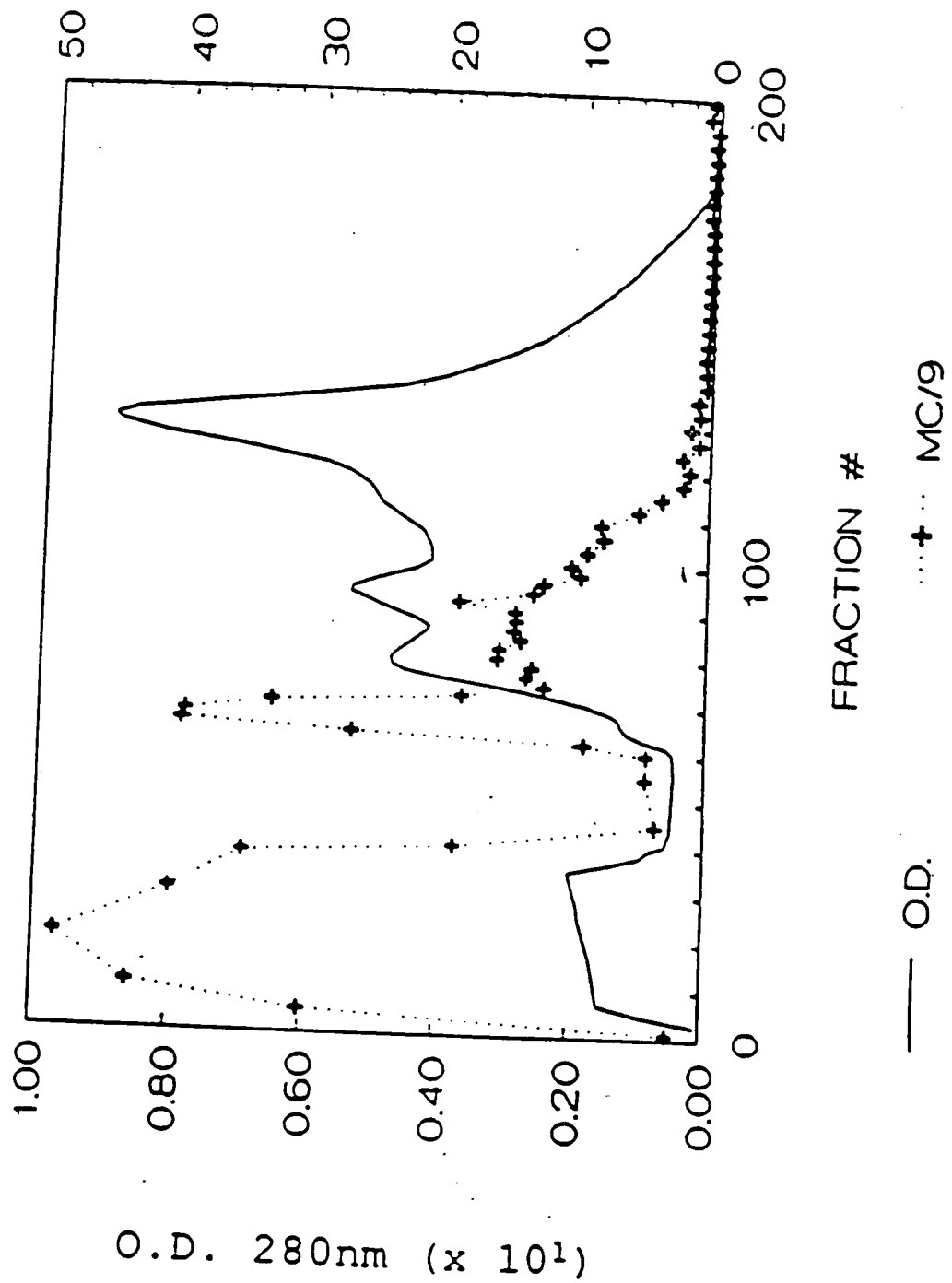


FIG. 5

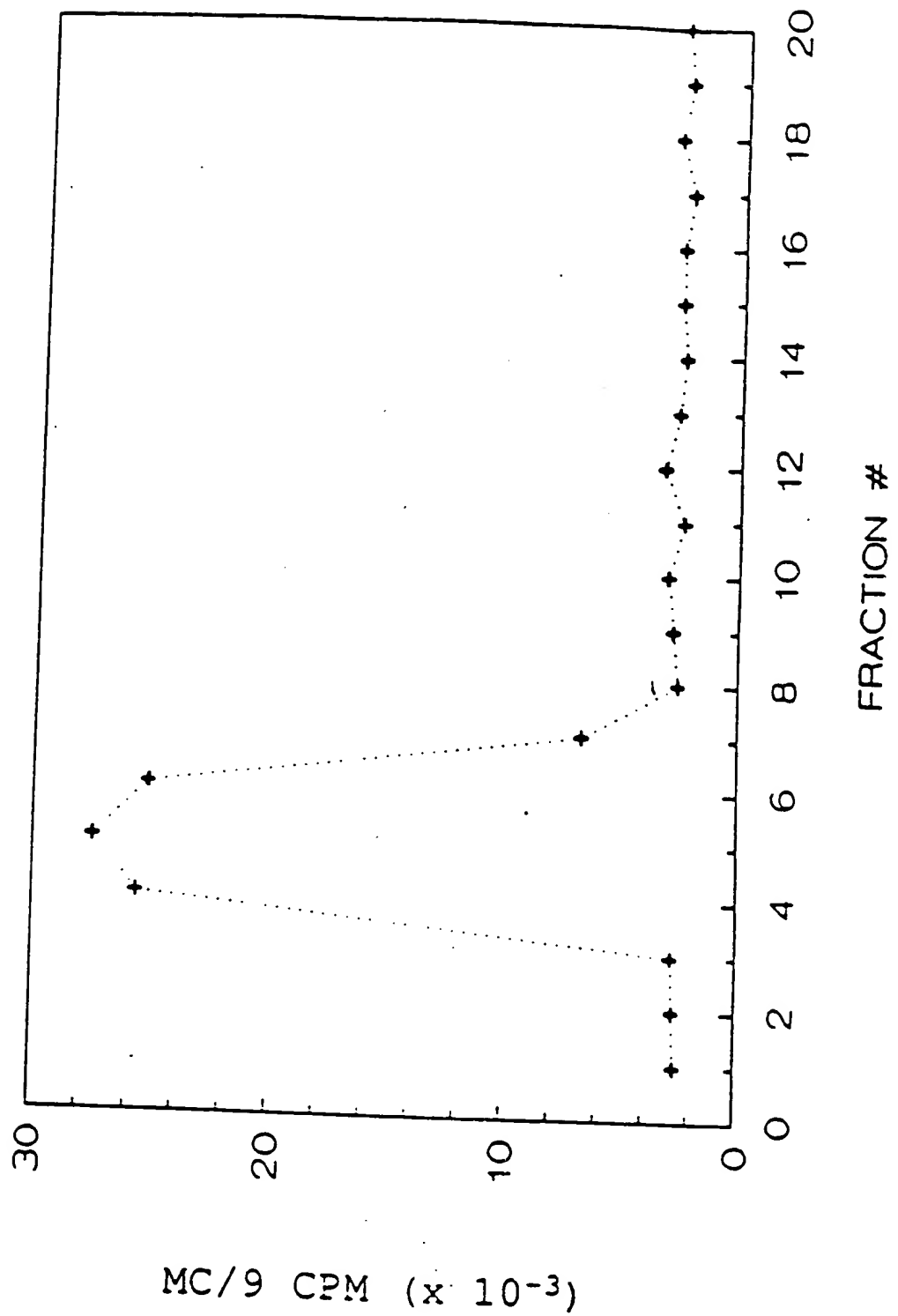


FIG. 6

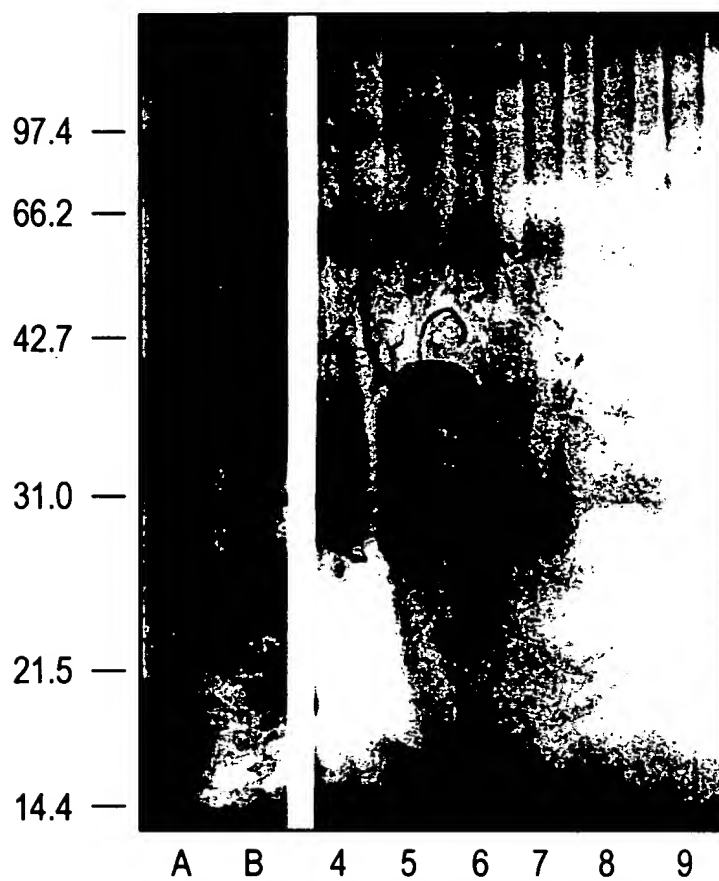


FIG. 7

MC/9 CPM

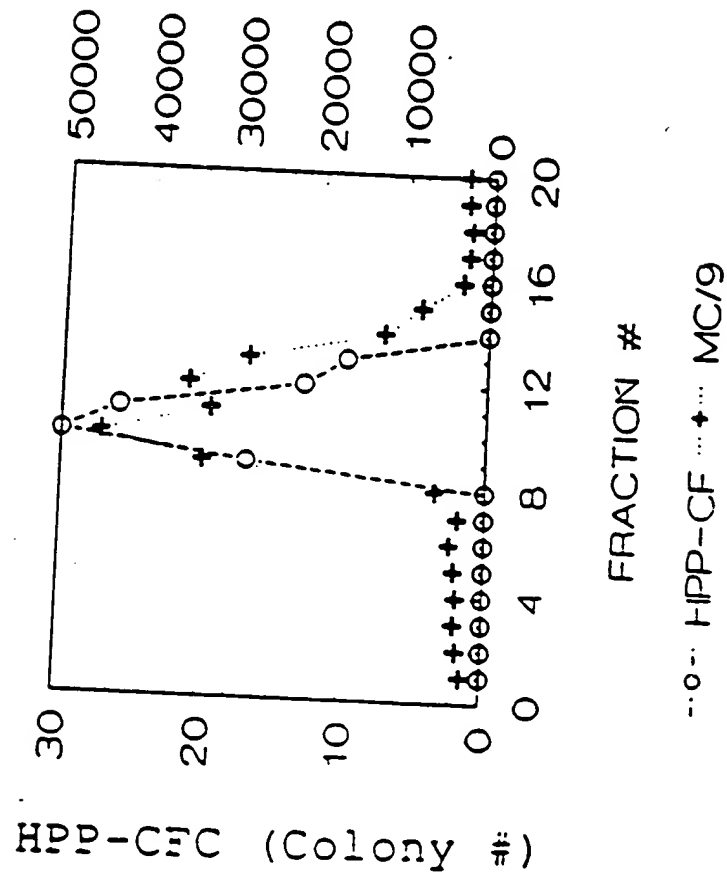


FIG. 8

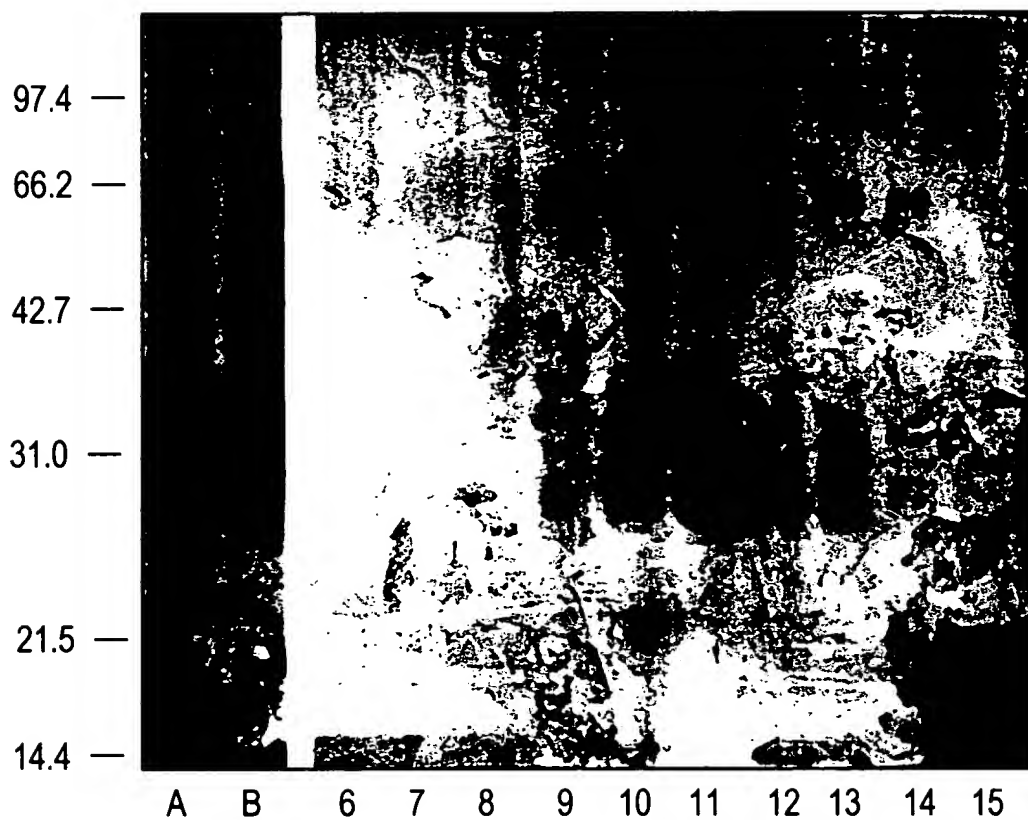


FIG. 9

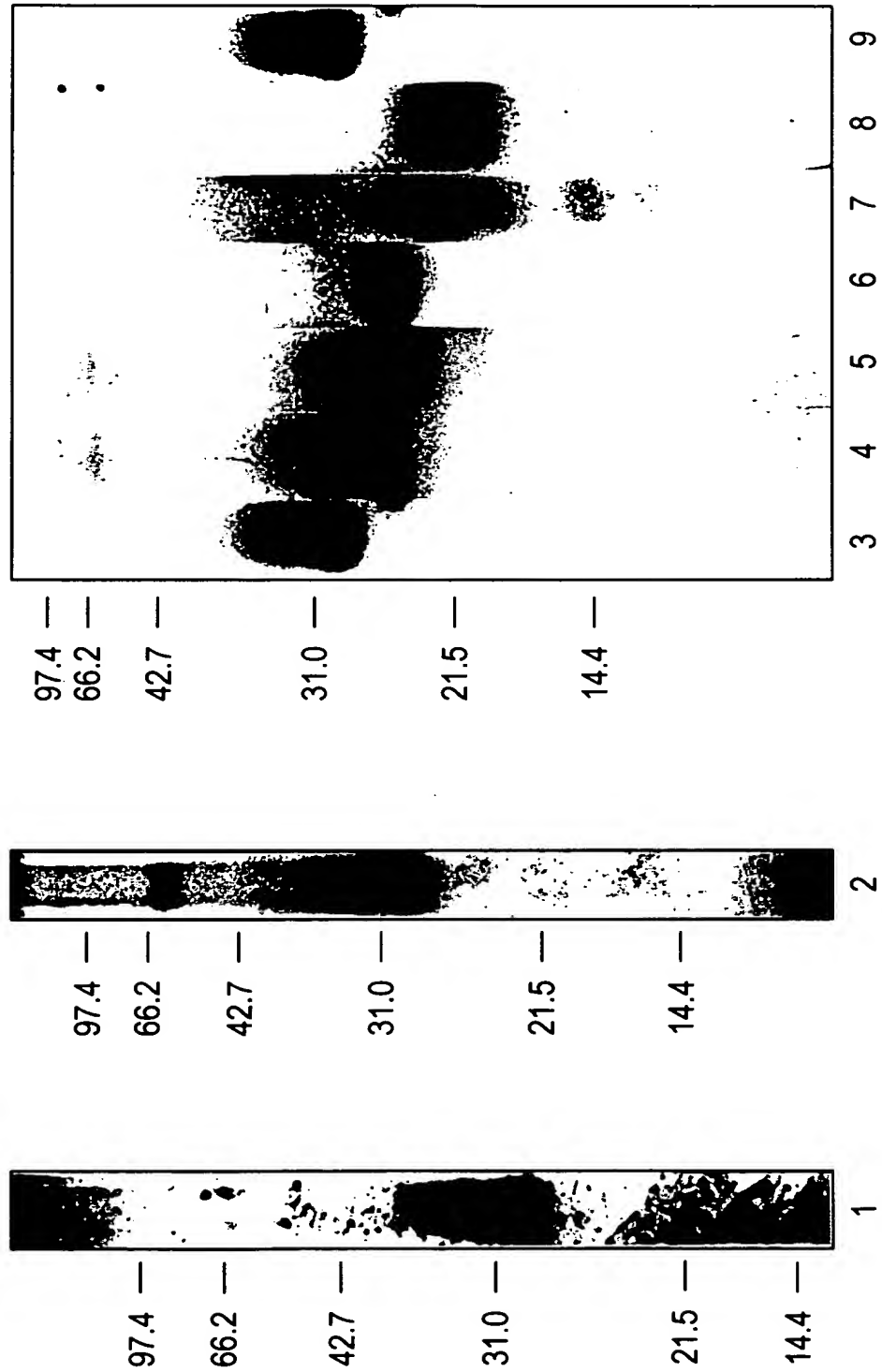


FIG. 10

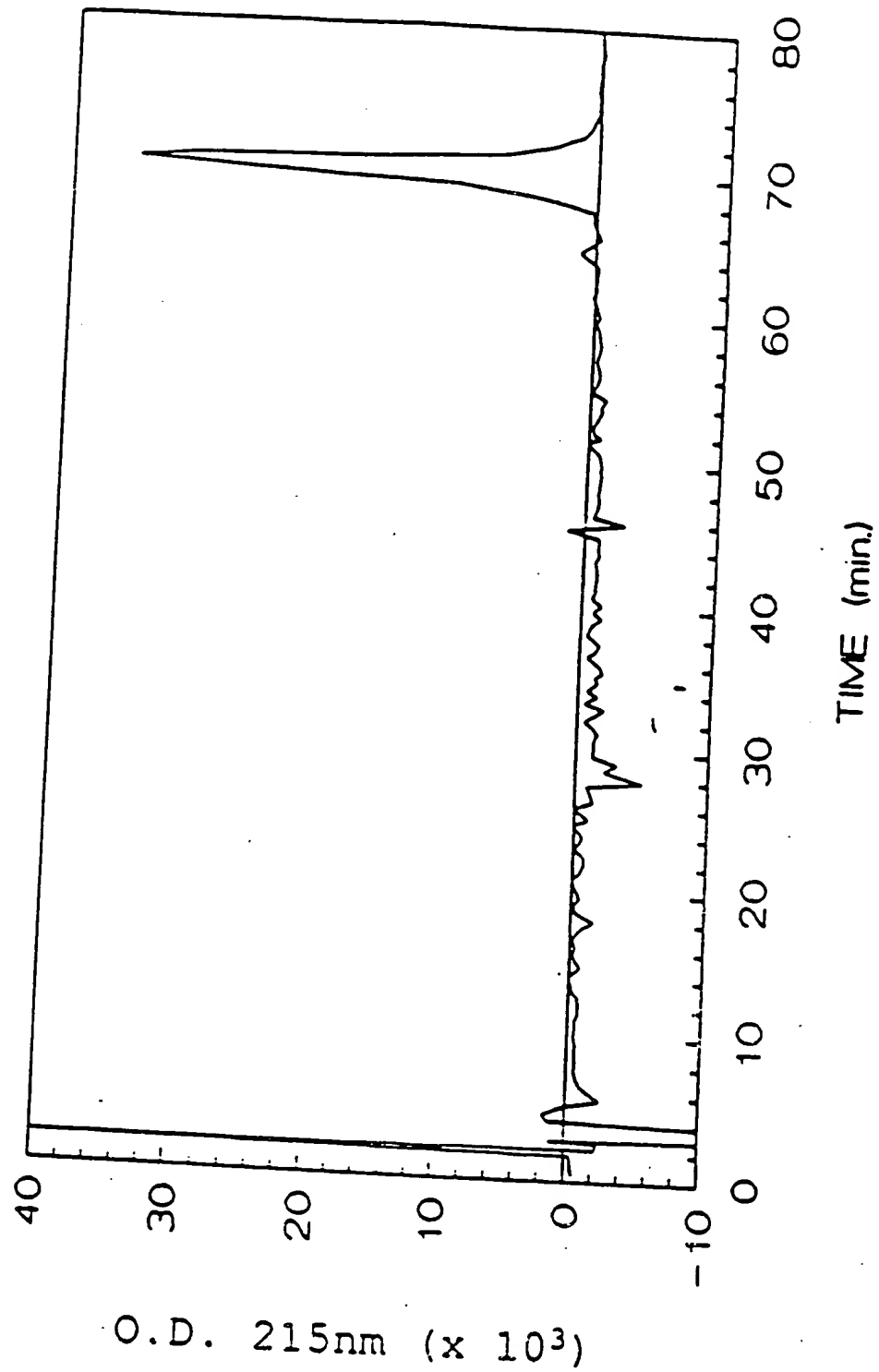


FIG. 11

1 10 20
pE E I C R N P V T D N V K D I T K L V A N L P N D
----- Sequencing after
----- T-5a -----
30 40 50
Y M I T L N Y V A G M D V L P S H C W L R D M V T
<Glu Aminopeptidase Treatment ----->
----- T-5a -----
----- CB-6a ----- CB-8; CB-10 -----
60 70
H L S V S L T T L L D K F S N I S E G L S N Y S I
----- Sequencing after Trp Cleavage -----
80 90 100
I D K L G K I V D D L V A C M E E N A P K N V K E
----- T-3 -----
----- CB-14; CB-15; CB-16 -----
----- S-1 -----
110 120
S L K K P E T R N F T P E E F F S I F N R S I D A
--- T-1 ----- T-4 (N109 nonglyco) -----
----- T-7 (N120 glyco); T-8 (N109 nonglyco) -----
----- CB-14; CB-15; CB-16 -----
----- S-5 or S-6 (N109 nonglyco) -----
130 140 150
F K D F M V A S D T S D C V L S S T L G P E K D S
----- T-5b -----
----- CB-6B -----
----- S-5 or S-6 -----
160
R V S V T K P F M L P P V A(A)
----- T-2 ----- (Carboxypeptidase)
----- CB-6B -----
----- S-2 -----

FIG. 12A-1

OLIGO	SEQUENCE	LOCATION
219-21	ACATTCTTIGGIGCATTCCTCCTCAT G T G T T	393-368
219-22	AAAACTCCTCIGGIGTAAATT G T T G G	447-425
219-25	GTTTCNGGTTTTT C C C	420-407
219-26	ATGGAAGAAACGCCCCCAAACGT G G T G T	368-393
222-11	CCNAATGATTATATGATAAC C C C C T	167-186
222-12	GGNGGNAACATAAANGGCTT G G T	566-585
223-6	ACCATAAAATCTTTAAACGATC G G C G G	492-470
224-24	GTATTTTCAATAGATCCATTGA	450-471
224-25	CCAACTATGTCGCC	190-202
224-27	GTAGTCAAGCTGACTGATAAG	273-253

FIG.12A-2

224-28	TAACCAACAATGACTAGGCAA	235-215
225-31	TTCCAGAGTCAGTGTC	547-562
227-29	GCGAAGCTTGCCCTTCCCTTATGAAGAAGA	16-35 *
227-30	GCGCCGCGGTACGGTGGTAACATGAAGGGCTTTGTGA	586-561 *
228-30	GATAAATGCAAGTGATAATCC	45-65
230-25	GCGGTCGACCCGCGGAACCTTAAAGTCCATGCAACAC	705-685 *
237-19	CACCCGCGGTTATGCAACAGGGGGTAACATAAATGG	569-592 *
237-20	CACCCGCGGTTAGGCTGCAACAGGGGGTAACATAAA	572-595 *

FIG.12B

OLIGO	SEQUENCE	LOCATION
231-27	CTTAATGTTGAAGAAACC	703-686
233-13	GATGGTAGTACAATTGTCAGAC	410-431
233-14	GTCTGACAATTGTACTACCATC	431-410
235-29	CAATTTAGTGACGTCTTTTACA	302-323
235-30	TTAGATGAGTTTTCTTTCACGCAC	556-533
235-31	AAATCATTCAAGAGCCCAGAACCC	566-589
236-31	AACATCCATCCCGGGGAC	366-383
238-31	CTGGCAATATTTTAAGTCTCAAGAAGACC	
241-6	GCGCCGCGGCTCCTATAGGTGCTAATTGG	
254-9	CCTCACCACCTGTTTGTGCTGGATCGCA	153-179
262-13	GGTGTCTAGACTTGTGTCTTCTTCATAAGGA	209-190

FIG.12C

OLIGO	SEQUENCE
201-7	CCCCCCCCGG T A
220-3	TTTTTTTTTTTTTTTTTTGG
220-7	TTTTTTTTTTTTTTTTTTAG
220-11	TTTTTTTTTTTTTTTTTTTCG
221-11	TTCGGCCGATCAGGCCCCCCCCCCC
221-12	TTCGGCCGGATAGGCCTTTTTTTTTTTTTT
228-28	GGCCGGATAGGCCTCACNNNNNNT
228-29	GGCCGGATAGGCCTCAC

FIG. 13A

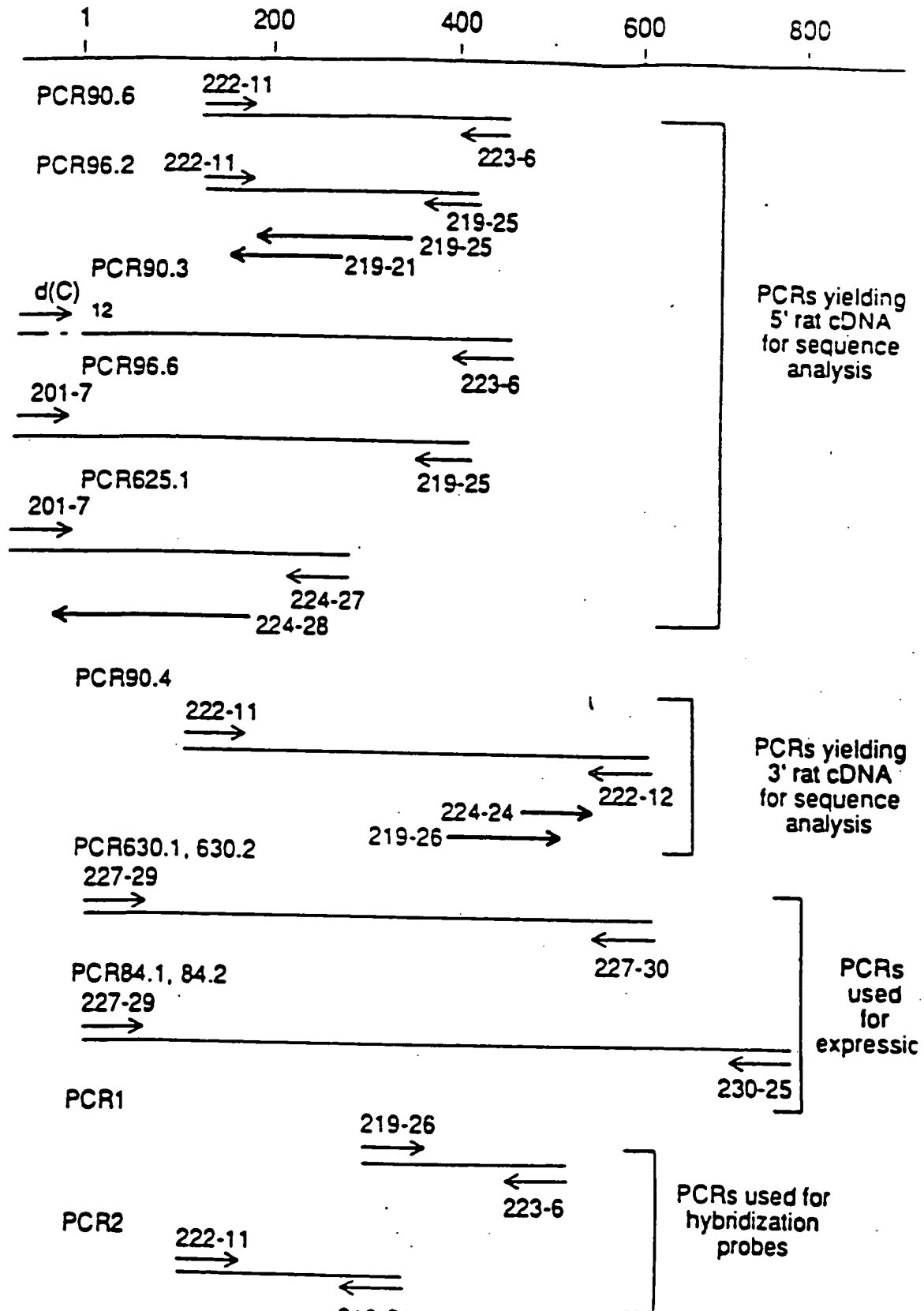


FIG. 13B

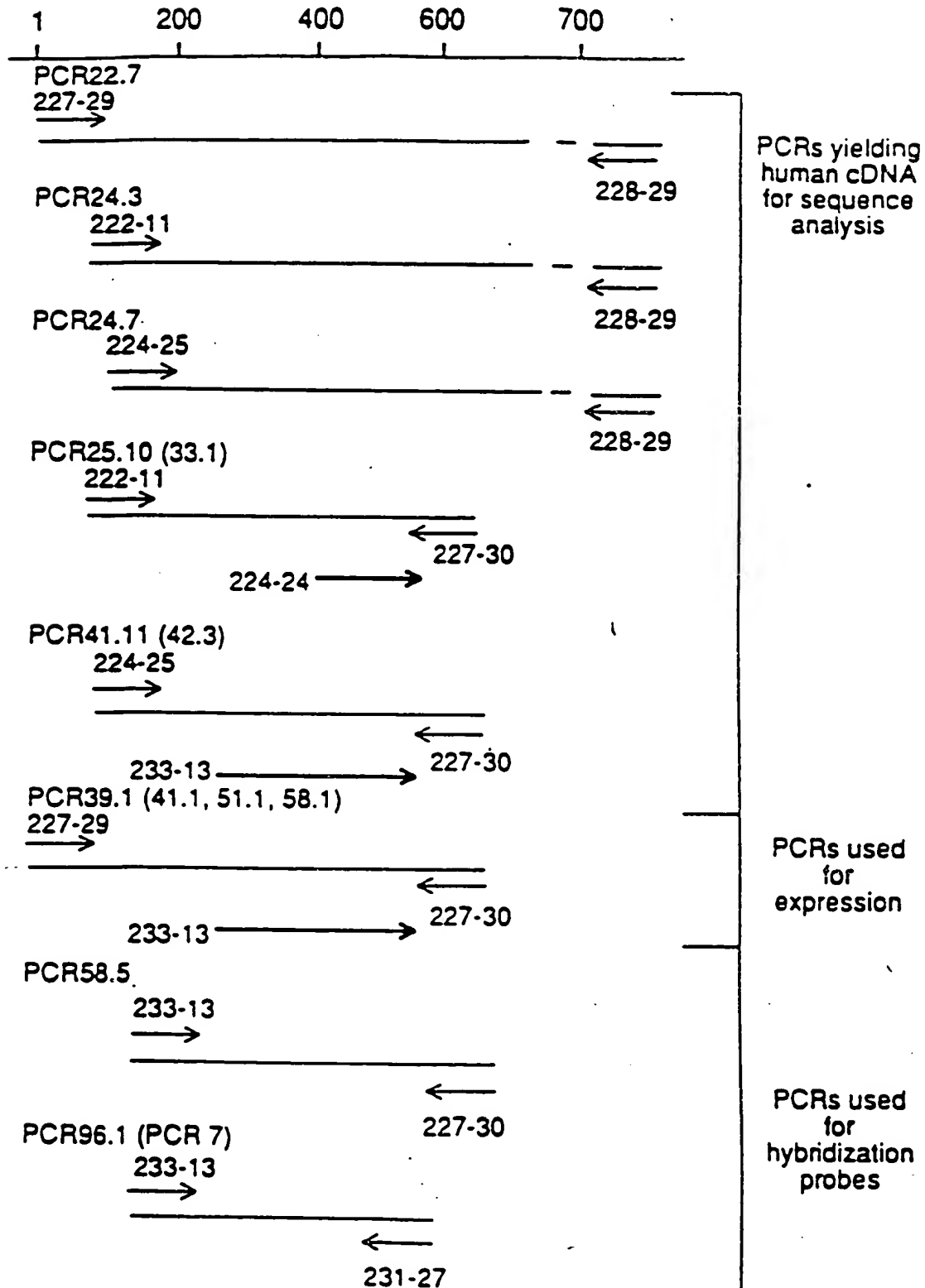


FIG. 14A

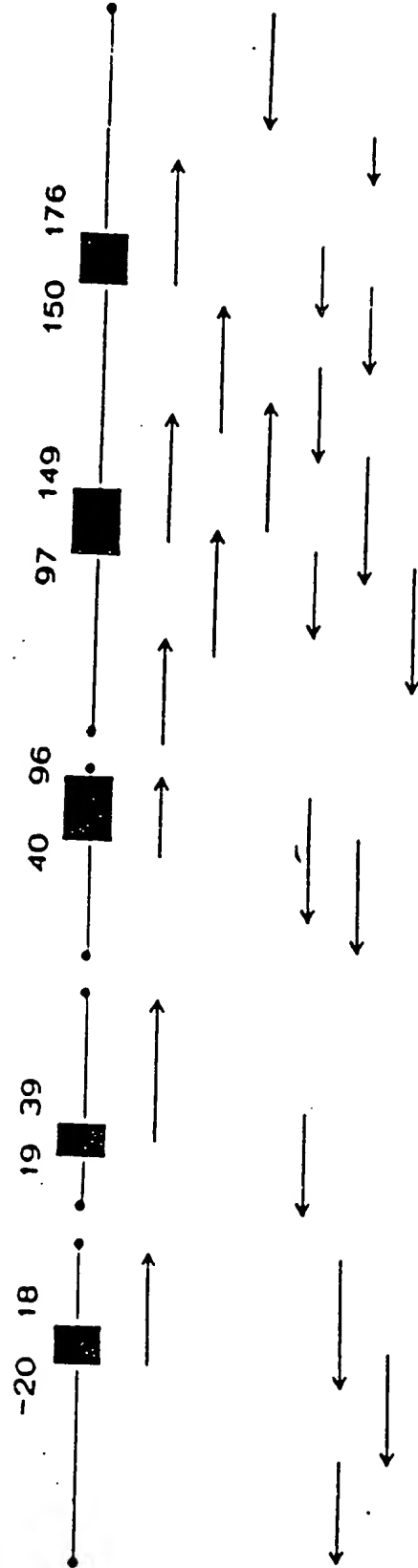


FIG.14B-1

AAAGTATCTTTCTATTGGCGAAGGACATGTTTTCCcATAAGTGGT	45
AAACA _n ACTGTCTGCACATAATAATTATCTTGCTGCCGTAAAGAT	90
TAGGTTAAATTCTGcCTTCGATCTAAAAACACACCCTTCTGTCAA	135
TCCGAGGAGCAGTGTGCTAGTCTAGAGGTCTAAATGAAGGCTCCT	180
TTCACGGTTGTATTTCTGCTCCCCAAATTGTCCACATTTAAAAGG	225
AGAGTGCTTCTTTTCAGCCTTAGGCTCTGAATTTTCATGCATTTCCT	270
CCATTTTCCGAGGTCCCcCcC _c AAGTGATAATTCTGTTACACGTTG	315
CTACAAGTTCATCCCTAATTGCCGTCAAGAACTGACTGTAGAAG	360
GCTTACCACAGACGTTGTAACCGACAGTAAAGCCATTGAAAGAGT	405
AATTCAAACAGGATGGAAGCCAGGAGTATTTTGTGGCTGTTGCTC	450
TTTTTCTTTTCAGTTTGGTGAGAGCAGCTTGAATGCTTAACATTT	495
AAGCCATCAGCTTAAACAAAACAAAACAAAACAAAAAAAACCC	540
CGCTCTGGCATATTTGCACTTAACACATACGGTATAAGGTGTTAC	585
TGGTTTGCATAGTTCTGGATTTTTTTTTTTTAA _{AA} ACTGATGGAC	630

-20

ThrT_rpIleIleThrC

ACCAAGAAATGTTTCTGTTCTTTGTTTAGACTTGGATTATCACTT	675
---	-----

-10

ysIleTyrLeuGlnLeuLeuLeuPheAsnProLeuValLysThrG	
GCATTTATCTTCAACTGCTCCTATTTAATCCTCTCGTCAAACTC	720

1

10

lnGluIleCysArgAsnProValThrAspAsnValLysAspIleT	
AGGAGATCTGCAGGAATCCTGTGACTGATAATGTAAAAGACATTA	765

FIG.14B-2

CAAACTGGTAAGTAAAGAATGATTTTGGCATCTATAAGTCTTCC	810
CTGTGCTTGCTGACCACATAGGTTTCAGGGCACTCCCGACAGGAGT	855
TCCCAGCTTTCTAAGATAAGGAATCACTGTACGAGTCTGAAGTGC	900
TTCTTCTGGGCAAATGGGAGATGCTTAGGTCATGGAGGGTTTATC	945
TGTATAACTGGCCCTTTGCACACCAACAAAGTGACTGACTGGCTT	990
TTGCCTGTTACCTACTG	1007

Intervening sequence of unknown length

TCTCCAGTCCTGGGCATGGTATATACTTAGGCACCCAAGATTGGA	45
TTTACAACTCAAGCATTATATATTGGACAACnACGGGGTATGAGA	90
TATTAATGATATGTCAGGTTGGATGGATGAGTTTTCTCAAGAAAT	135

19

Val

TCTCTTGTATTTACTCACGTTTTTCATTTCTTGGTCTCTGTAGGTG	180
--	-----

30

AlaAsnLeuProAsnAspTyrMetIleThrLeuAsnTyrValAla	
GCGAATCTTCCAAATGACTATATGATAACCCTCAACTATGTCGCC	225

39

GlyMetAspValLeu

GGGATGGATGTTTTGGTATGTAGTCCACACACTTCTGAGTTGCCT	270
---	-----

TTTAGTAGCTAATGGGTGACCTGTGCTTATTCACATTGAAGACAT	315
---	-----

TATTTGCTCTTTGTCGTTTTTAGATGTTGACCTATAATTTTTCCT	360
---	-----

TCAAGCTGCTGCTAAGATTATCAGTGAGCATTTCAGTATGTGTTT	405
---	-----

TTTCCCTACTGCTTTTAAAGCAATGGCGTCTCTTACAGCTTCCCT	450
---	-----

FIG.14B-3

CCGATGTTAATTTTTTCCCCAGGCATCTCTCAGAGGGACTTGAATG 495
TTAAAATCATGTAAATTTCTCCTTGGCTATGTTATTTCTCATG 540
GCTATGTTATTCCTATTCGTATTTCAATTTAAAGGGACGGAATATT 585
TATTGTATTTCTGAACTTTTTTCAGGCATGCATCCGGGTCTTTGAA 630
TAAAA 635

Intervening sequence of unknown length

CACTAAGACTCCTTCTAGTAATGTTTGTAATCCTGTCTGTATCGA 45
ATGTCTTTGAAAACGCAGTGACTAAGCCATAAATAATCTTCCACA 90
GAACGTCCAGTGGTTCATGAACTTTGTATGTGGGGGTGGGGCAAG 135
AATTGTCTCACTATTGGTCAAGGAAGAGAAGGTAAGGTATGCAAG 180
GGTGGTTTAATCTTCTTCCGTGGAAGGACAAAATCATCTATCATT 225
TCCTCTGATCTCTATGCATTTGTTTGTTTTGAACTGAATCTGACT 270
TGAGCAAGAGTTGGCGTCCTGTGTTCTGAGGAACTCTTTGTCTCT 315
GCAGTCAGTGACTAAAAGTGCTGAGAGATCTGAAGAGCACTCTGA 360
ATCTGCCATATTTTTTAATAGATGCTTTGTCTTCTCTTTGAATTTC 405

40.

50

ProSerHisCysTrpLeuArgAspMetValThrHisLeu
TTCCAGCCTAGTCATTGTTGGTTACGAGATATGGTAACACACTTA 450

60

SerValSerLeuThrThrLeuLeuAspLysPheSerAsnIleSer
TCAGTCAGCTTGACTACTCTTCTGGACAAGTTTTCAAATATTTCT 495

70

80

GluGlyLeuSerAsnTyrSerIleIleAspLysLeuGlyLysIle

FIG.14B-4

GAAGGCTTGAGTAATTATTCCATCATAGACAAACTTGGGAAAATA 540

90 96
ValAspAspLeuValAlaCysMetGluGluAsnAlaProLys
GTGGATGACCTCGTGGCATGTATGGAAGAAAATGCACCTAAGGTA 585

ACTTGGTATTCATCAGAATTATTTTTCTTATACT 619

Intervening sequence of unknown length

GAGCTCATGATGAGCAATTCACAACCACTTGTAATTCCAGCTCCA 45
GAGGACATTATCCCCTCCTTGGATGCCATAGGAATCTGCTCTCAA 90
ATATGTAGATAACCACTCTGCCACCTCAGCACATACATACACATA 135
ATTAAAAAATAGAAACATTAAAGGAGTTCCAATCAATCCTTATTC 180
TTTTCTGTATTCAGTATGCCCAGATGTAAATTCTAGGAATATGTT 225
TTAAAGGCTAATTCTTATTTTGTAAATAAGCAGCTTTAAAATTCTT 270
AATTGTTTTTTTCGGGTCACCTTTATTGTCCTATTGCCACGACATTG 315
TCCTGTCCCATTTGTCTGTTATTCCTTCTGTTTTGTTTATTGTTCC 360
CTAGTTACTTTGATCATGAGATTGACCTGTTACCCGTTGTTATTC 405
TCTGTAGCCATTTTGAGTTGTGTCTATTAGAACAGCTGTAAATT 450
ACTTGAATCATTGAGGACATAGTCAATAATCTATTATGCTGATCC 495
AGTCAAGTCTATGAGTTATTTGAAAAC TAGAATCTTTGTTAATTA 540

97
AsnValLys
TTTGTTTGCTTGTTTGTTTGTTTATTATTTGTCTAGAATGTAAAA 585

100 110
GluSerLeuLysLysProGluThrArgAsnPheThrProGluGlu

FIG.14B-5

GAATCACTGAAGAAGCCAGAACTAGAACTTTACTCCTGAAGAA 630

120

PhePheSerIlePheAsnArgSerIleAspAlaPheLysAspPhe
TTCTTTAGTATTTTCAATAGATCCATTGATGCCTTCAAGGACTTC 675

130 140

MetValAlaSerAspThrSerAspCysValLeuSerSerThrLeu
ATGGTGGCATCTGACACTAGTGATTGTGTGCTCTCTTCAACATTA 720

148

GlyProGluLysA
GGTCCTGAGAAAGGTAAGGCTTTTAAGCATTTCTTGTTTAAATGT 765

ACATAGAAAGCCTGAACTTCTGTAAGCCTCTACTGCTGAATCAAC 810

TAAATGTGTTGCTGTAGAAAGAACGTGTGGGTTTTTCTGATAAAA 855

ACAAAAAGCAAATATCAATGACTACCAATGATTATTATCTAGCTT 900

GAGAGATATGCCCTAAGACAGCGATTCTCGATATTTCTAAATTAA 945

AGAATTGTGTGATGGTGGCTCACATATTTTCTAACTGTGATATTT 990

GCCAGGAGAGTAGAATAATGTTATTCTTCATCCCCAGAATTCCTA 1035

AGATTTACGTCTCATGTCTTTTCCATAAGGTTCAAACCTCTGAGA 1080

CTTGAGTTCTGAGCCTCAGCAGGTCATTCTGAATCCCCACTCTCC 1125

CCGAGCTGGGTCCCTATGGGGGAACTAACTTCATTGCTTTCTTTT 1170

AAAACATGACGAGTTACCAACAGCTCCTCGCTATTATAAACATGT 1215

TCCTAAGCATGTCTGTGCATGCATAAGCCTTCACTCTACAAGAC 1260

AGTTATGGTGTATCGCTTGACAAAACCTGAGCAGCCAAGCTGAGTA 1305

TGAAATAATAATCTAGACTTGGGAGGCAGACCCAGCACCTACTGT 1350

GATATTGCACTTCGCCTTTGGGGGACTCTATGATTCAAAAGTTCA 1395

FIG.14B-6

150
spSerArgV
CCATGTAACTGACACATTATTGCTTTCTATTAGATTCCAGAG 1440

160
alSerValThrLysProPheMetLeuProProValAlaAlaSerS
TCAGTGTCACAAAACCATTTATGTTACCCCCTGTtGCAGCCAGTT 1485

170 176
erLeuArgAsnAspSerSerSerSerAsn_
CCCTTAGGAATGACAGCAGTAGCAGTAATAGTAAGTACACATATC 1530

TGATTTACTGCATGCATGGCTCCAAGTATCCTCTATAGGAGTGTT 1575

GCATGGACTTAAAGTTTATAAATCACTACTAATAATGCTGTTCTG 1620

TCAGTGTTATTCCTTGTATGGGCTTCCTGACAATTAAATATCTGG 1665

TTTGTAGAATCGGATCTCCTTAGAGGTTAAGATGACCATGACAAA 1710

ATTAGGCCAATCAACTTTCTGCGAAGGTTATTTTAAATAAGGCAC 1755

GAAATTAATTGAAGGAAAAAAAAAATACAAGCAAGGCCTTATTTTG 1800

AATCATGGTAGGCTTAAATAGACTTTGTGGAGAATGTCCCTGAT 1845

CAAAGTGGAGTTTTTCAGATTTCAAGTGCATGTGCTAACTCTCCAC 1890

AATGTCAAGGCTATTTTCAGTTTTGTGTCTCCATATTTACTACTG 1935

CATGTTTGGAAATTTGCTGATGCTGTTAGATTACCTAAGAATGTA 1980

TGTTGAAGAAGAATGGACTTCTTTCCCTAAAATTTCTGTCCTCTT 2025

TGcCCAAGAACCCAcGTTCCCTGGAAGACTATCTTATTTTCATGTC 2070

TGTGCAATGATCATTATAAAGATTATTGAATATACTGGGAATACT 2115

CTGGTTTCTGTTTTTACAGATTCATAATAGCTTATTCAGTCTTTA 2160

AAGAAAGTTCTCTGAAGTCCATGCCTTTAGAATGTTTCTCTATCAA 2205

FIG.14B-7

AACTTGACCTGGACCTTAAATAAAGCTATATTTAGTCTTTTTATC	2250
CCTGAAAAATATATTTACAGTGTAGACATTTGATATACATCTAA	2295
GGGAAGGATGCTGCCAGAATGCTCGGGCTGGCAGTCTACAAAGTC	2340
CACTGCTCTCAGGATGGACTTCTGAAAGCGGAAATTGTGAACTGC	2385
ATGCATATAACATATCAGATCCTCGAGC	2413

FIG.14C-1

```

-25      -20
M K K T Q T W I I T C I
CTGGATCGCAGCGCTGCCCTTTCCCTTATGAAGAAGACACAACTTGGATTATCACCTGCAT 60

-10      1
Y L Q L L L F N P L V K T Q E I C R N P
TTATCTTCAACTGCTCCTATTAAATCCTCTCGTCAAAACTCAGGAGATCTGCAGGAATCC 120

10      20
V T D N V K D I T K L V A N L P N D Y M
TGTGACTGATAATGTAAAGACATTACAAACTGGTGGCGAATCTTCCAAATGACTATAT 180

30      40
I T L N Y V A G M D V L P S H C W L R D
GATAACCCCTCAACTATGTGCGCGGATGGATGTTTTGCCTAGTCATTTGTTGGTTACGAGA 240

50      60
M V T H L S V S L T T L L D K F S N I S
TATGGTAACACACTTATCAGTCAGCTTGACTACTCTTCTGGACAAGTTTTCAAATATTTC 300

70      80
E G L S N Y S I I D K L G K I V D D L V
TGAAGGCTTGAGTAATTATTCATCATAGACAACTTGGGAAAATAGTGGATGACCTCGT 360

90      100
A C M E E N A P K N V K E S L K K P E T
GGCATGTATGGAAGAAATGCACCTAAGATGTAAAGAATCACTGAAGAAGCCAGAAC 420

110      120
R N F T P E E F S I F N R S I D A F K
TAGAACTTTACTCCTGAAGAATTCTTTAGTATTTTCAATAGATCCATTTGATGCCTTCAA 480
```

FIG.14C-2

130 D F M V A S D T S D C V L S S T L G P E
140 GGACTTCATGGTGGCATCTGACACTAGTAGTGTGTGCTCTCTTCAACATTAGGTCCTGA 540
150 K D S R V S V T K P F M L P P V A A S S
160 GAAAGATTCCAGAGTCAGTGTCAAAACCATTATGTATACCCCTGTTCAGCCAGTTC 600
170 L R N D S S S N R K A A K S P E D P G
180 CCTTAGGAATGACAGCAGTAGCAGTAATAGGAAAGCCGCAAGTCCCTGAAGACCCAGG 660
190 L Q W T A M A L P A L I S L V I G F A F
200 CCTACAATGGACAGCAATGGCACTGCCGGCTCTCATTTGCGCTTGTAATTGCGCTTGCTTT 720
210 G A L Y W K K K Q S S L T R A V E N I Q
220 TGGAGCCTTATACTGGAAGAAGAAACAGTCAAGTCTTACAAGGGCAGTTGAAATATACA 780
230 I N E E D N E I S M L Q Q K E R E F Q E
240 GATTAAATGAAGAGGATAATGAGATAAGTATGTTGCAACAGAAAGAGAGAGAGTTCAGA 840
248 V
GGTGTAAAT 849

FIG. 15A

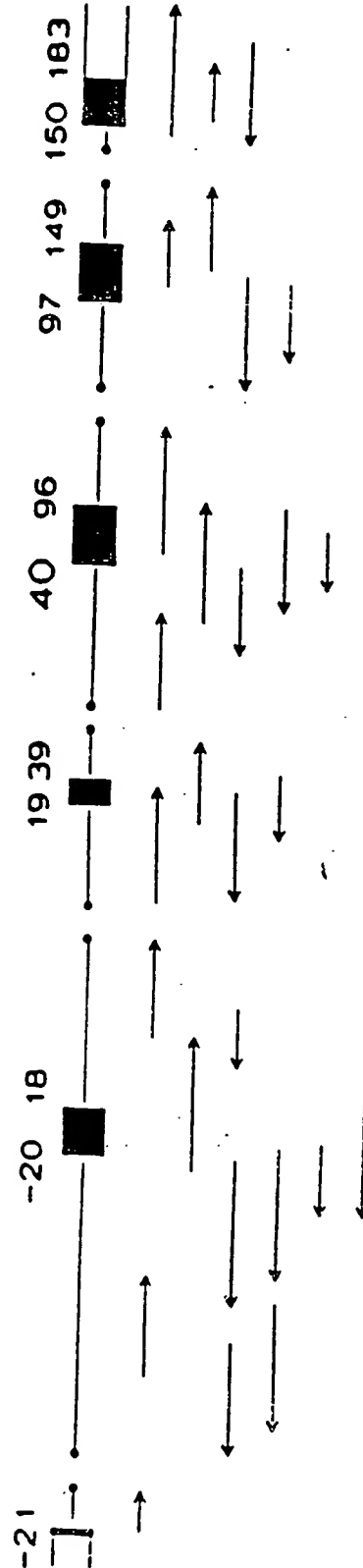


FIG.15B-1

-21
hrGln

CACAAGTGAGTAGGGCGCGCCCGGGAGCTCCCAGGCTCTCCAGGA 45
AAAATCGCGCCCGGTGCCCGGGGAGCCGGCGCTCCCTGGGACT 90
TGCAGCTGGGGCGTGCAGGGCTGTGCCTGCCGGGTG 126

Intervening sequence of unknown length

AGATACTACAAAGATAAATCAGTTGCACAAGTTCTTGAAACTCTA 45
CAGTGTAATAAGGAAAAATAAGTCATGCATAAAAGCAACTATAAT 90
ACATAATAGAAAATGTTATTTTCAAGCCGATGTGTAGGTTATGTG 135
TGTTTCGAGAGAGAGAGAGAGAAGACAGATTACTTTCTGCTAGGGT 180
TCAAGAATGCCTTCCTGTTGGCTAAGGAAATATTTTCCTTAAGTG 225
GCTAAAAAGCTGTGTTTCAAATATTCTTTTGATGTCTCACAAAT 270
TCAGTGGAATTCTCTTAGGTCTAAAAATATACATCTCTCTCACTT 315
TAACTTGGTGTGCTATTGTAGATTATTGGATTAAAGCACTGCTCA 360
GGGATTATGCTGCTTCTTGCCAAGCAGTCTACATTTAAAGTAGAA 405
ATAAGATGTTTCTTTTGGTGCCATAAGGTATACATTTTATGCATT 450
CTCTAGTTTTTTAGAAGATACCCTAAGGGCTAAGTCTTTAACATGC 495
TGCTACAAGTTTATTCCCTAATTGCCATTGGGAAATTGGCTGAAGA 540
AAGTTTTTTAACAAAAGTTAACAATATTGTCATTGAGAGAATAATT 585
CAAAATGGATTTTAACTAAAAGCTTTTAAAAACTTTGGTGAGCAT 630
AGCTTGAATGCGTAATATTTAATTGCATTTAAGCCAATAACATAT 675

FIG.15B-2

ATTAGACTGGTCTTTTTGTGCATCAAGGCATTAGATGTTAAAAGT	720	
TTGAATGATTACAGATCTTAAGTATGATCACCAGCAATTTTTC	765	
<div style="display: flex; justify-content: space-between; width: 100%;"> -20 -10 </div> <div style="text-align: center; margin-bottom: 5px;"> ThrTrpIleLeuThrCysIleTyrLeuGlnLe </div> <td>TGTTTTCATTTAGACTTGGATTCTCACTTGCATTTATCTTCAGCT</td> <td>810</td>	TGTTTTCATTTAGACTTGGATTCTCACTTGCATTTATCTTCAGCT	810
<div style="text-align: center; margin-bottom: 5px;">1</div> <td>uLeuLeuPheAsnProLeuValLysThrGluGlyIleCysArgAs</td> <td></td>	uLeuLeuPheAsnProLeuValLysThrGluGlyIleCysArgAs	
GCTCCTATTTAATCCTCTCGTCAAACTGAAGGGATCTGCAGGAA	855	
<div style="display: flex; justify-content: space-between; width: 100%;"> 10 18 </div> <td>nArgValThrAsnAsnValLysAspValThrLysLeu</td> <td></td>	nArgValThrAsnAsnValLysAspValThrLysLeu	
TCGTGTGACTAATAATGTAAAAGACGTCATAAATTGGTAAGTAA	900	
GGAATGCTTTACCGTGCTGTGTAAAAAGAGCTGTGGCTCTTTTT	945	
CCTGTGCTTGTTGATAAAAGATTTAGATTTTTCTTGCCCCAAAGT	990	
AATGTTTTCTTAAAGTGGGGAAAGTAATCACTGGGTACAATAAA	1035	
GGGTTTATAGAAAGCAGGTAGTGAGATATTTAGGGTCATGGATAA	1080	
TTTGTTGGTAAAACTGGCTAGTTGCACACCACTGCTGTGACTGCT	1125	
TCTTTGCTGGTCTTCTCCCCATCCTTCATAGGCAGTGAAGGACCT	1170	
TGGAGAGTTCGCTGTGTGCTGATGGGCTTGCCCCAGCTTGTTCCC	1215	
CATAATCTCTCCAGTGGGTTTCCCAGCATGTTCTATTCCCCTTCA	1260	
CATGTCTTCCTACTCTTCTTTAAAAAGCCTAACGAAAGGAAATCT	1305	
GAAATGGCTATTCTCCCAATTCAATCAGCAGGAAGACCCTGTCAC	1350	
ATGTCAGTGGGTGTTTGCTCCTTCAGGGAACATAGAGAGGTGATT	1395	
CATTGCCACATGTTGAAGGGACTCATCTCCCTGGTTTGTACAT	1440	
TGAACTCTTCCTCAGCGAAAGCATTTCATTGCTTCCC	1479	

FIG.15B-3

Intervening sequence of unknown length

GAATTCCAAGATCACAGGTGGAAGCTGAAATTCAGATCATGTTTC	45
CAAACCTCAGTAGGTTATACCTAGCCAGGCATAACTGAATTTGGA	90
GTCTAAAAGATCTGTATTATCACTTTTTTTATTTTGAAGGATGCCT	135
TTTGATTACAGAGGGGAAATCAAGGATTAAAAATCAATATACATGT	180
AAATATTGAAATTCATTGGTAACTTTAAAAAGCACAACAGTTTTG	225
TGTGCTTTTCTCCAAAGCACTACAAATATGATTAATTGATGTATA	270
	19
	ValAlaA
AGAATTTTCTTATGGAATTTTTTTTTTTTGTCTCTGTAGGTGGCAA	315
	30
snLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyM	
ATCTTCCAAAAGACTACATGATAACCCTCAAATATGTCCCCGGGA	360
	39
etAspValLeu	
TGGATGTTTTGGTATGTAACTACATTTCTGAGTTTCATTTTAGT	405
AGCTCATAGAAGAAATGGGATCATTATATTGAGATAGTACACTA	450
GCTGCTATTTAGGAGCTTGCTTATTGTCAGGATTTGAAGAATTTA	495
TCTTTGGAATTTGACTTGCAGGCTTTTTTTTCCCCCTCTT	535

Intervening sequence of unknown length

CCTGTTACAAGAGTCCCTCCTCCTATTAGAATAGTCCCTCCTCCT	45
CCTGTCACACTAGTCCCTTCTCTTCCTGTTACAATAACCCCTGTC	90

FIG.15B-4

CTCCTATTACAACATTTTAAAGTAATGTAATATTAATTTTAAAAAT 135
CTGGCCAGGCACGGTGGTTCATGCTTGTAATCCCAGCACATTGGG 180
AAGCTGAGACGGGTGGATCATTGAGGTCAGGAAGTTTGAGACAG 225
CCTGGCCAACATGGTGAACTTCCTCTCTACTAAAAATAAAAAAG 270
TAGCCAGGCATGGTGGCAGGCACTTGTAATCTGAGCTACTCGAGA 315
GGCTGAGGCAGGAGAATCACTTGAGTAACTAAAACGATAGCTTTG 360
AAGAGTACTCCGAGTTTTATGGCACTTACTTATTAAAATAGCTGT 405
40
ProSerHisCysTrpIleS
TTTGTCTCTTTTTTTCATATCTTGCGAGCCAAGTCATTGTTGGATAA 450
50 60
erGluMetValValGlnLeuSerAspSerLeuThrAspLeuLeuA
GCGAGATGGTAGTACAATTGTCAGACAGCTTGACTGATCTTCTGG 495
70
spLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleI
ACAAGTTTTCAAATATTTCTGAAGGCTTGAGTAATTATTCCATCA 540
80 90
leAspLysLeuValAsnIleValAspAspLeuValGluCysValL
TAGACAAACTTGTGAATATAGTGGATGACCTTGTGGAGTGCGTGA 585
96
ysGluAsnSerSerLys
AAGAAAACCTCATCTAAGGTAACCTTGTGTTCATTGGGATTATTTT 630
TCATTACGCTTCTCTAAAAACCCATGCTTCTTGGTGCTGTTGGGG 675
AAAATGAGGCACCTTTATTTATGATATTTTGATTGTATAAACTTC 720
AAATTTAAAAATCTTGTTTCAGATGAGCAAAGAAAACAAGTATTTG 765
CAGTTATACTGCAATACTGAAGTGCACATTC 796

FIG.15B-5

Intervening sequence of unknown length

TTGTGTTCACTGCCCCAGATTCAACTTGTGATCCCACTGGGATCA	45
CTACCCTGCATTACCAATCTGAATTACATACGTTAAACAGCCAT	90
CTAAAAGTGCTAGTTGTAAGAGTCTAAATACTTGAATCTTTGAGA	135
GACATATTTATAGTCCATTATCTTCACCTCAGTTAAGTCTGAAGA	180
97	
CTATTTGAAAAATGTAATCCTATTTTTTCTTCTAGGATCTAAAAA	225
110	
ysSerPheLysSerProGluProArgLeuPheThrProGluGluP	
AATCATTCAAGAGCCCAGAACCCAGGCTCTTTACTCCTGAAGAAT	270
120 130	
hePheArgIlePheAsnArgSerIleAspAlaPheLysAspPheV	
TCTTTAGAATTTTTAATAGATCCATTGATGCCTTCAAGGACTTTG	315
140	
alValAlaSerGluThrSerAspCysValValSerSerThrLeuS	
TAGTGGCATCTGAACTAGTGATTGTGTGGTTTCTTCAACATTAA	360
148	
erProGluLysA	
GTCCTGAGAAAGGTAAGACATGTAAGCATTTCAGTTCAAATGTA	405
AACAACAAACTTAAATCTTCCCTATGTAGTAAGAATCTACCTCTG	450
TGTTAAGCTGTAGCAAGATACATGCATGTACGTCTAATAAAAAAG	495
CAGATATCAATAGCACAGAAGAAA	519

Intervening sequence of unknown length

FIG.15B-6

CTCTATAACTCATACAAATCACCATATAACACTGACACATTATTG 45

150 160
spSerArgValSerValThrLysProPheMetL
CTTTCTATTTAGATTCCAGAGTCAGTGTCACAAAACCATTTATGT 90

170
euProProValAlaAlaSerSerLeuArgAsnAspSerSerSerS
TACCCCCTGTTGCAGCCAGCTCCCTTAGGAATGACAGCAGTAGCA 135

176
erAsnA
GTAATAGTAAGTACATATATCTGATTTAATGCATGCATGGCTCCA 180

ATTAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAACTTCT 225

ACATTTATTATTATTGATACTGTTCTGTTACTGTTATTCCTTTTA 270

TGGTCTTCTTGAGACTTAAGTTTGTAGAATTAAATTTCCCTAGAG 315

CTGGAGATAATGTTT TAGAGAATTAGGCCAATAAATTT 352

FIG.15C-1

```
-25      -20
M K K T Q T W I L T C I Y L Q
AAGCTTGCCTTTCCTTATGAAGAGACACAACTTGGATTCTCACTTGCAATTATCTTCAG 61

-10      1
L L L F N P L V K T E G I C R N R V T N
CTGCTCCTATTAACTCCTCGTCAAACTGAAGGATCTGCAGGAATCGTGTGACTAAT 121

      20      30
N V K D V T K L V A N L P K D Y M I T L
AATGTAAGACGTCACATAAATTGGTGGCAAACTCTTCCAAAAGACTACATGATAACCCCTC 181

      40      50
K Y V P G M D V L P S H C W I S E M V V
AAATATGTCCCGGATGGATGTTTGGCCAAAGTCATTGTTGGATAAGCGAGATGGTAGTA 241

      60      70
Q L S D S L T D L L D K F S N I S E G L
CAATTGTCAGACAGCTTGACTGATCTTCTGGACAAGTTTTCAAATATTCTGAAGGCTTG 301

      80      90
S N Y S I I D K L V N I V D D L V E C V
AGTAATTATCCATCATAGACAACTTGTGAATATAGTGGATGACCTTGTGGAGTCCGTG 361

      100      110
K E N S S K D L K K S F K S P E P R L F
AAAGAAACTCATCTAAGGATCTAAAAAATCATTTCAAGAGCCCCAGAACCCAGGCTCTTT 421
```

FIG.15C-2

120
T P E E F F R I F N R S I D A F K D F V 130
ACTCCTGAAGAATTCTTTAGAAATTTTAAATAGATCCCATTTGATGCCCTTCAAGGACTTTGTA 481

140
V A S E T S D C V V S S T L S P E K D S 150
GTGGCATCTGAAACTAGTGATTGTGGTTTCTTCAACATTAAAGTCCCTGAGAAAGATTCC 541

160
R V S V T K P F M L P P V A A S S L R N 170
AGAGTCAGTGTCAACAACCATTTATGTATGTTACCCCTGTGTCAGCCAGCTCCCTTAGGAAT 601

180 183
D S S S N S K Y I Y L I
GACAGCAGTAGCAGTAATAGTAAGTACATATATCTGATTAAATGCATGCATGGCTCCAAT 661

TAGCACCTATAGGAGTATTGCATGGGCTTCAAGGAAACTTCTACATTATTATTATTGA 721

TACTGTTCTGTACTGTTATTCCTTTTATGGTCTTCTTGAGACTTAAGTTGTAGAAATTA 781

AATTCCCTAGAGCTGGAGATAATGTTTAGAGAATTAGG 820

FIG.15D-1

GAGCTCCGAGCCCTCtCTGGCGCgCgAGGTATTTTCGTCTGTnCCCCGGGGTGCCAGGTGA 60
GCCCCAGCGGATCCGGGAGGGTAAGCTGGGACTCCTCGCGAGCAGTAGCTGCAGGGTACC 120
AAGCTTCGCCCTCTGCGTCCCCCGCCCTTCGCGGTCTCCCCGCCAGTGCAGGTCCGGGGCC 180
CCCAGCGAGCGGACAAAGTTGGCCCTAATCTGCCAACACTTCTGGGGCATTTACCGTGCTC 240
TGGCCGCCCTCCCCGATTCTTCCCTCCGGCCCTTGCCCTGCTTCTCGCCTACCCCGGGCTC 300
CGGAAGGGAAGGAGGCGTGTCCGGAGCAGCGGGCGGGAACTGTATAAAGCGCCGGCGG 360
CTCAGCAGCCGGCTTCGCTCGCCGCCCTCGCGCCGAGACTAGMAGCGCTGCGGGNAGCAGG 420
GACAGTGGAGAGGCGCTCGGCTCGGGCTACCCCAATGCGTGGACTATCTGCCGCCCGCTGT 480
TCGTGCACATCTCTGGAGCTCCAGMACAGCTAACGGAGTCGCCACACCACTGTTTGTGC 540

-25 -21
Met Lys Lys Thr Gln
TGTATCGCTCTCTGCTTTCCTTATGAAAGAGACACAAAGTAGTAGGGCGGCCCGGGA 600
GCTCCCAGGCTCTCCAGGAAATACTCGCGCCCGGTGCCCGGGNAGCCGGCGCTCCCTGG 660
GACTTGACGCTCGGGCGTGCAGGGCTGTGCTGCCGGGTGAGACAAGAGGATGCGGGGGA 720
GGCCGGCGTGGTGTGATCCCCGAGCCGAGCCGnTGAGCCAGGGAGAAAGAGTGGA 780
GTnCTGAGAGGGAGCCAGTGTCAAGTTTGGAGCCTCAGCAGTTAAGTTTTGAGCTGTCAG 840
TCGGAACCCGTAATCCCCGCTCTGGTGGAAAGATTGGCTTTTnGCCACGGAATGTAAGTT 900
ATCAC 905

FIG.15D-2

Intervening sequence of unknown length

AGATACTACAAAGATAAATCAGTTGCACAGTTCTTGAACTCTACAGTGTAATAAGGAA	60
AAATAAGTCATGCATAAAAGCAACTATAAÇATAATAGAAAATGTTATTTTCAAGCCGA	120
TGTGTAGGTTATGTGTGTTCCGAGAGAGAGAGAGACAGATTACTTTCTGCTAGGGT	180
TCAAGAATGCCTTCCGTTGGCTAAGGAAATATTTTCCTTAAGTGGCTAANAAGCTGTGT	240
TTCAAAATATTCTTTTGATGTCTCACAAATTCAGTGGAAATCTCTTAGGTCTAANAATAT	300
ACATCTCTCTCACTTTAACTTGGTGIGCTATTGTAGATTATTGGATTAAAGCACTGCTCA	360
GGGATTATGCTGCTTCTTGCCMAGCAGTCTACATTTAAGTAGNATAAGATGTTTCTTT	420
TGGTGCCATTAAGGTATACATTTTATGCATTCTCTAGTTTATAGAAATACCCCTAAGGGCT	480
AAGTCTTTAACTATGCTGCTACAAAGTTTATTCCTAATTGCCATTGGGNAATTGGCTGAAGA	540
AAGTTTTTTAAVAAAGTTAACAAATATTGTCATTGAGAGAAATAATTCNAAATGGATTTTAA	600
CTAAAGCTTTTAAAACTTTGGTGAGCATAGCTTGAATGCGTAATATTTAATTGCATTT	660
AAGCCAAATAACATATATAGACTGGTCTTTTGTGTCATCAAGGCATTAGATGTTAAAGT	720
TTGAATGATTACAGATCTTAACTGATGATCACCAAGCAATTTTCTGTTTTCATTTAGAC	780
	-20
	Th
rTrpIleLeuThrCysIleTyrLeuGlnLeuLeuLeuPheAsnProLeuValLysThrG1	
TTGGATTCTCAGCTTGCAATTTATCTTCAGCTGCTCCTATTATTAATCCTCTCGTCAAAACTGA	840

FIG.15D-3

1 10 18
uGlyIleCysArgAsnArgValThrAsnAsnValLysAspValThrLysLeu
AGGATCTGCAGGAATCGTGTGACTAATAATGTAAAGACGTCACATAATTGGTAAGTAA 900
GGAATGCTTTACCGTGTGTAAAGAGAGCTGTGGCTCTTTTCCCTGTGCTTGTGTGAT 960
AAAAGATTTAGATTTTCTTGCCCCAAAGTAATGTTTTCCTAAAGTGGGGAAAGTAATCA 1020
CTGGGTTACAATAAAGGGTTTATAGAAAGCAGGTAGTGAGATATTTAGGGTCATGGATAA 1080
TTTGTGGTAAACTGGCTAGTTGCACACCACTGCTGTGACTGCTTCTTTGCTGCTCTTC 1140
TCCCCATCCTTCATAGGCAGTGAAGGACCCTTGAGAGAGTTCGCTGTGTGCTGATGGGCTTG 1200
CCCCAGCTTGTTCCTCCATAATCTCTCCAGTGGGTTTCCCAGCATGTTCCTATTCCTCCCTCA 1260
CATGTCTTCTTACTCTTCTTTTAAAGCCTAACGAAAGGMAATCTGAAATGGCTATTCTC 1320
CCAAATTCAAATAGCAGGMAAGACCCTGTCACATGTCAGTGGGTGTTTGCCTCCTTCAGGGAA 1380
CATAGAGAGAGTATTCATTGCCCCACATGTTGAAGGGACTCATCTCCCTGGTTTGTACAT 1440
TGAAC'TCTTCCC'TCAGCGMAAGCATTTGCAATTGCTTCCC 1479

Intervening sequence of unknown length

GAATTCCAAGATCACAGGTGGAAGGTGMAATTCAGATCATGTTCCAAACTCAGTAGGT 60
TATACCTAGCCAGGCATAACTGAATTTGGAGTCTAAAGATCTGTATTATCACTTTTTTA 120
TTTTGAAGGATGCCCTTTTGATTACAGAGGGGAAATCAAGGATTAAAAATCAATATACATGT 180

FIG.15D-4

```

AAATATTGAAATTCATTGGTAACCTTTAAANAAGCACACAGTTTTGTGTGCTTTTCTCTCCAA 240
AGCACTACAAATATGATTTAATTGATGTATAGAATTTTCTTATGGAATTTTTTTTTTTGTGT 300
ValAlaAsnLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyM
CTCTGTAGGTGGCAAAATCTTCCAAAAGACTACATGATMAACCCTCAAAATATGTCCCCGGGA 360
etAspValLeu
TGGATGTTTTTGGTATGTAAACTACATTTCTGAGTTTTCATTTTAGTAGCTCATAGAGAAA 420
TGGGATCATATTTGAGATAGTACACTAGCTGCTATTTTAGGAGCTTGCTTATTGTCTAG 480
GATTTGMAAGNAATTTATCTTTTGGMAATTTTGACTTGCAGGCTTTTTTTTCCCCCTCTT 535
Intervening sequence of unknown length
CCTGTTACAAATATTTCCCTCCTCCTATTACANTAGTCCCTCCTCCTGTCACTAGTG 60
CCTTCTCTTTCTGTTACAAATAAACCCTGTCTCCTATTACAAACATTTTAAGTAATGTAAT 120
ATTAATTTTAAAAATCTGGCCAGGCACGGTGGTTTCATGCTTGTAATCCCAGCACATTTGGG 180
AAGCTGAGACGGGTGGATCATTTGAGGTCAGGAAGTTTGAGACAGCCTGGCCAAACATGGT 240
GAAACTTCCTCTCTACTAAAAATAAAAAAGTAGCCAGGCATGGTGGCAGGCACCTTGTAAT 300
CTGAGCTACTCGAGAGGCTGAGGCAGGAGAAATCACTTGAGTAACATAAACGATAGCTTTG 360
AAGAGTACTCCGAGTTTTTATGGCACTTACTTATTAAAAATAGCTGTTTTGTCTCTTTTTC 420
```


FIG.15D-5

40	ProSerHisCysTrpIleSerGluMetValValGlnLeuSerAspSerL	50	
	ATATCTTGCAGCCCAAGTCATTGTTGGATNAGCGAGATGGTAGTACAAATTGTCAGACAGCT		480
60			
	euThrAspLeuLeuAspLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleI	70	
	TGACTGATCTTCTGGACAAAGTTTTTCAMATATTTCTGMAAGGCTTGAGTAATTATTCCATCA		540
80			
	leAspLysLeuValAsnIleValAspAspLeuValGluCysValLysGluAsnSerSerL	90	
	TAGACMAACTTGTGAATATAGTGGATGACCTTGTGGAGTGGTGMAAGMAAATCATCTA		600
96			
ys	AGGTAACTTTGTGTTTCATTGGGATTATTTTTTCATTACGCTTCTCTMAAAACCCATGCTTC		660
	TTGGTGCTGTTGGGGAAATGAGGCACCTTTATTTATGATATTTTGTGATTGTATAAACTTC		720
	AAATTTAAAAATCTTGTTCAGATGAGCMAAGMAACMAAGTATTTCAGATTATACTGCAAT		780
	ACTGMAAGTGCAATTC		796
	Intervening sequence of unknown length		
	TTGTGTTCACTGCCCCAGATTCAACTTGTGATCCCACTGGGATCACTACCCCTGCATTACC		60
	AATCTGAATTACATACGTTAAACACAGCCATCTAAAGTGCTAGTTGTGAAGAGTCTAAATA		120
	CTTGAATCTTTGAGAGACATATTTATAGTCCATTATCTTCACCTCAGTTAAGTCTGAAGA		180
	97		
	AspLeuLysLysSerPheLysSerP		240
	CTATTTGAAAAATGTAATCCTATTTTTTCTCTAGGATCTAAAAAATCATTTCAAGAGCC		

FIG.15D-6

```

110      roGluProArgLeuPheThrProGluGluPhePheArgIlePheAsnArgSerIleAspA
120      CAGAACCCAGGCTCTTTACTCTCTGAGAAATCTTTAGAAATTTTAAATAGATCCATTTGATG
300
130      laPheLysAspPheValValAlaSerGluThrSerAspCysValValSerSerThrLeuS
140      CCTTCAAGGACTTTGTAGTGGCATCTGAACTAGTGATTGTGTGGTTTCTTCAACATTAA
360
148      erProGluLysA
      GTCCCTGAGAAAGGTAAGACATGTAAGCATTTCCAGTTTCMAATGTMAACAACTTAA
420
      TCTTCCCTATGTAGTAAGAAATCTACCTCTGTGTGTTAAGCTGTAGCAAGATACATGATGTA
480
      CGCTAATAAAGCAGATATCAATAGCACAGMAGAACTAATGATTGTAGATTTGTGGG
541
      Intervening sequence of unknown length

      CTCTATATACCAATCACCATATACACTGACACATTTATTGCTTTCTATTAGATT
60      spS
150      erArgValSerValThrLysProPheMetLeuProProValAlaAlaSerSerLeuArgA
      CCAGAGTCAGTGTACAAAACCATTTATGTTACCCCTGTTCAGCCAGCTCCCTTAGGA
120
170      snAspSerSerSerSerAsnA
      ATGACAGCAGTAGCAGTAATAGTAAGTACATATATCTGATTTAATGCATGCATGGCTCCA
180
      ATTAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAACTTCTACATTTATTATTATT
240
      GATACTGTTCTGTACTGTATTCTTTTATGGTCTTCTTGAGACTTAAGTTTGTAGAA
300
```

FIG.15D-7

```
TAAATTTCCCTAGAGCTGGAGATAATGTTTAGAGAAATTAGGCCAATAAATTTTCTGCTGA 360
GGTTATTTTAAATAAGACATATAAATAATTTTAGAAATATGATTTATGCCCTTTTGTGAA 420
TCATTAACATATAT 434

Intervening sequence of unknown length

ACAGAAACAGTTAAACAACCCACAGCATAGAGGAAACTTCTAGAATGGATATGCTGTA 60

TTCATCAGTGTGTTCTTTTAAATTTATAGGGAGGCCAAATAATCCCCCTGGAGACTCCAGCC 120
190
eullisTrpAlaAlaMetAlaLeuProAlaIleuPheSerLeuIleIleGlyPheAlaPheG
TACACTGGCCACACCATGGCATTTGCCAGCATTTGTTTCTCTTATAAATTGGCTTTGCTTTTG 180
200
lyAlaLeuTyrTrpLys
GAGCCTTATACCTGGAAGGTAAAGTGGTACCATTCCCTTTTAAATAATATGCTATGTTTAC 240
ATAAATTATCATCTTTTTTTCCTCAAGAAATGATCCTTTAAGAAACAGTGAATCTACCT 300
TAGCTTATACTAAACAAAATTTAAATTTTATAAAGTTTCCCTGTTTCTCATTTATGCTCTGGA 360
GACAATCCCCTCTAGCTGATAATTACGCTTAAGAATTAGGAAC 404

Intervening sequence of unknown length
```

FIG.15D-8

AAAACTGTTATTGGAGTTATTGCCATAAAGATAAAGTGGAGTCCACTTACCTCTTAA	60
	214
TATTAGACCATTCATTGATTATTTTACAGTATATGTCTTTCTTCTTTTCCAGAAGAGAC	120
	LysArgG
	220
InProSerLeuThrArgAlaValGluAsnIleGlnIleAsnGluGluAspAsnGluIles	235
AGCCAAGTCTTACAAGGGCAGTTGAAATATACAAATTAATGAAGAGGATAATGAGATAA	180
	e
GGTATTTTGTGTTTGGCTAAATGTGTGCCCAATCAAGCATGACATTGCCATTTTCACACACTG	240
TGTACCTGCCCATTAATGTCTTTAAAGMAGTCCTTCACTCATGACAGTAGCTCCTAACCCAGT	300
GAGTCCCAACTCTATCCATGTTTCTGTATGTCTCACTCTCTCTTC	344
Intervening sequence of unknown length	
GTATGTGTATATATCATATACAGAGAAAGAAATGTTTAACTACTTGGMAAGACTACCTTA	60
AGACAAATGAAGTCTTCCCTCTATAGTAATAAGAGGTAGGCTCCCCCATTCAT	120
TTTGCAATCTTCTGCTACTATATTACAGAAAGCTGCCCTTTACAAATGCCGAGATCATG	180
GTGTACCTCAGAAATCTCTGACCAAGAGCAATAAGCATTTTCTTATTTGTTTTCAGTA	240
	rM
	237
etLeuGlnGluLysGluArgGluPheGlnGluVal	248
TGTTGCAAGAGAAAGAGAGAGAGTTTCAAGAGTGTAAATGTGGCTTGTATCAACACTGT	300
TACTTTCGTACATTGGTAAGTTTTTTTCTCTTTTCCCTTTTCTTTTCTTTTATATA	360

FIG.15D-9

CTTTAAGTTCTAGGGTACATGTGCGCACATGTGCGAGGTTTGTACGTATGTTTACATGTGC 420
CATGTT 426

FIG.16A

-25
Human MKKTQTWILT C1YLQLLLEN PLVKTEGICR NRVTNNVKDV TKLVANLPKD 25
Monkey MKKTQTWILT C1YLQLLLEN PLVKTEGICR NRVTNNVKDV TKLVANLPKD
Dog MKKTQTWIIIT C1YLQLLLEN PLVKTGICG KRVTDDVKDV TKLVANLPKD
Cat MKXTQTWIVT C1YLQXLLLEN PLVKTGICR NRVTDDVKDV TKLVANLPKD
Cow MKKTQTWIIIT C1YLQLLLEN PLVHTQGICS NRVTDDVKDV TKLVANLPKD
Rat MKKTQTWIIIT C1YLQLLLEN PLVKTQEICR NPVTDNVKDI TKLVANLPND
Mouse MKKTQTWIIIT C1YLQLLLEN PLVKTREICG NPVTDNVKDI TKLVANLPND
Chicken TWIIIT CFCLQLLLEN PLVKAQSSCG NPVTDDVNDI AKLVGNLPND
Scfpep MKKTQTWIIIT C1YLQLLLEN PLVkt.gicr nrvtd.vkdv tklvanlpkd

26
Human YMITLKYVPG MDVLP SHCWI SEMVQLSDS LTDLLDKFSN ISEG...LSN 72
Monkey YMITLKYVPG MDVLP SHCWI SEMVQLSDS LTDLLDKFSN ISEG...LSN
Dog YKIALKYVPG MDVLP SHCWI SVMVEQLSVS LTDLLDKFSN ISEG...LSN
Cat YKIALKYVPG MDVLP SHCWI SVMVEQLSVS LTDLLDKFSN ISEG...LSN
Cow YMITLKYVPG MDVLP SHCWI SEMVEQLSVS LTDLLDKFSN ISEG...LSN
Rat YMITLNYVAG MDVLP SHCWL RDMVTHLSVS LTDLLDKFSN ISEG...LSN
Mouse YMITLNYVAG MDVLP SHCWL RDMVIQLSLS LTDLLDKFSN ISEG...LSN
Chicken YLITLKYVPG MDVLP SHCWL HLMVPEFSRS LHNLLQKFSN ISEG...LSN
Scfpep YmitLkYVpg MDVLP SHCWI semveqlsvs ltdlldkfsn iseg...LSN

73
Human YSIIDKLVNI VDDLVECVKE NSSKD.LKKS FKSPEPRLET PEEFFRIFNR 121
Monkey YSIIDKLVNI VDDLVECVKE NSSKD.LKKS FKSPEPRLET PEEFFRIFNR
Dog YSIIDKLVKI VDDLVECTEG YSFEN.VKKA PKSPELRLET PEEFFRIFNR
Cat YSIIDKLVKI VDDLVECVKE HSEN.VKKS SKSPEPRLET PEEFFRIFNR
Cow YCIIDKLVKI VDDLVECMEX HSEN.VKKS SKSPEPRLET PEEFFRIFNR
Rat YSIIDKLVKI VDDLVECMEX HSEN.VKKS SKSPEPRLET PEEFFRIFNR
Mouse YSIIDKLVKI VDDLVECMEX HSEN.VKKS SKSPEPRLET PEEFFRIFNR
Chicken YSIIDKLVKI VDDLVECMEX HSEN.VKKS SKSPEPRLET PEEFFRIFNR
Scfpep YSIIDKLVKI VDDLVECMEX HSEN.VKKS SKSPEPRLET PEEFFRIFNR

FIG. 16B

122 Human SIDAfkDF.V VASeTSDCVV SSTL.SPEKD SRVSVTKPFM LPPVAASSLR 169
 Monkey SIDAfkDF.A VASeTSDCVV SSTL.SPEKD SRVSVTKPFM LPPVAASSLR
 Dog SIDAfkDLEt VASKSSECVV SSTL.SPDKD SRVSVTKPFM LPPVAASSLR
 Cat SIDAfkDLEM VASKTSECVV SSTL.SPEKD SRVSVTKPFM LPPVAASSLR
 Cow SIDAfkDLEI VASKMSECVI SSTL.SPEKD SRVSVTKPFM LPPVAASSLR
 Rat SIDAfkDF.M VASDTSDCVL SSTL.GPEKD SRVSVTKPFM LPPVAASSLR
 Mouse SIDAfkDF.M VASDTSDCVL SSTL.GPEKD SRVSVTKPFM LPPVAASSLR
 Chicken TIEVYREFAD SLDK.NDCIM PSTVETPEND SRVAVTKTIS FPPVAASSLR
 Scfpep eIdafkdf.m vasktdCvV SSTL.sPeKD SRVSVTKpfm LPPVAASSLR

170 Human NDSSSSNRKA KNPPGD.... ..SSLIWAAM ALPAFFSLII GFaFGALYWK 213
 Monkey NDSSSSNRKA KNPTGD.... ..SSLIWAAM ALPAFFSLII GFaFGALYWK
 Dog NDSSSSNRKA SNSIGD.... ..SNLQWAAM ALPAFFSLVI GFaFGALYWK
 Cat NDSSSSNRKX TNPIED.... ..SSIQWAVM ALPACFSLVI GFaFGAFYWK
 Cow NDSSSSNRKA SNSIED.... ..SSLQWAAV ALPAFFSLVI GFaFGAFYWK
 Rat NDSSSSNRKA AKSPED.... ..PGLQWTAM ALPALISLVI GFaFGALYWK
 Mouse NDSSSSNRKA AKAPED.... ..SGLQWTAM ALPALISLVI GFaFGALYWK
 Chicken NDIGSNTSS NSNKEALGFI SSSSLQGISI ALTSLLSLII GFILGAIYWK
 Scfpep NDSeSSNRka .n..ed.... ..eSLQWaaM ALpalfSLVI GFaFGALYWK

214 Human KRQPSLTRAV ENIQIN...E EDNEISMLQe KEREfQeV 248
 Monkey KRQPSLTRAV ENIQIN...E 'DDNEISMLQe KEREfQeV
 Dog KRQPNLTRTV ENIQIN...E EDNEISMLQe KEREfQeV
 Cat KRQPNLTRTV ENIQIN...E EDNEISMLQe KEREfQeV
 Cow KRQPNLTRTV ENRQIN...E EDNEISMLQe KEREfQeV
 Rat KRQSSLTRAV ENIQIN...E EDNEISMLQe KEREfQeV
 Mouse KRQSSLTRAV ENIQIN...E EDNEISMLQe KEREfQeV
 Chicken KTHPKSRPES NETIQCHGCQ EENEISMLQe KEREHLQV
 Scfpep Kkqpeltrav eniqin...e edNEISMLQe KEREfQeV

FIG. 16C

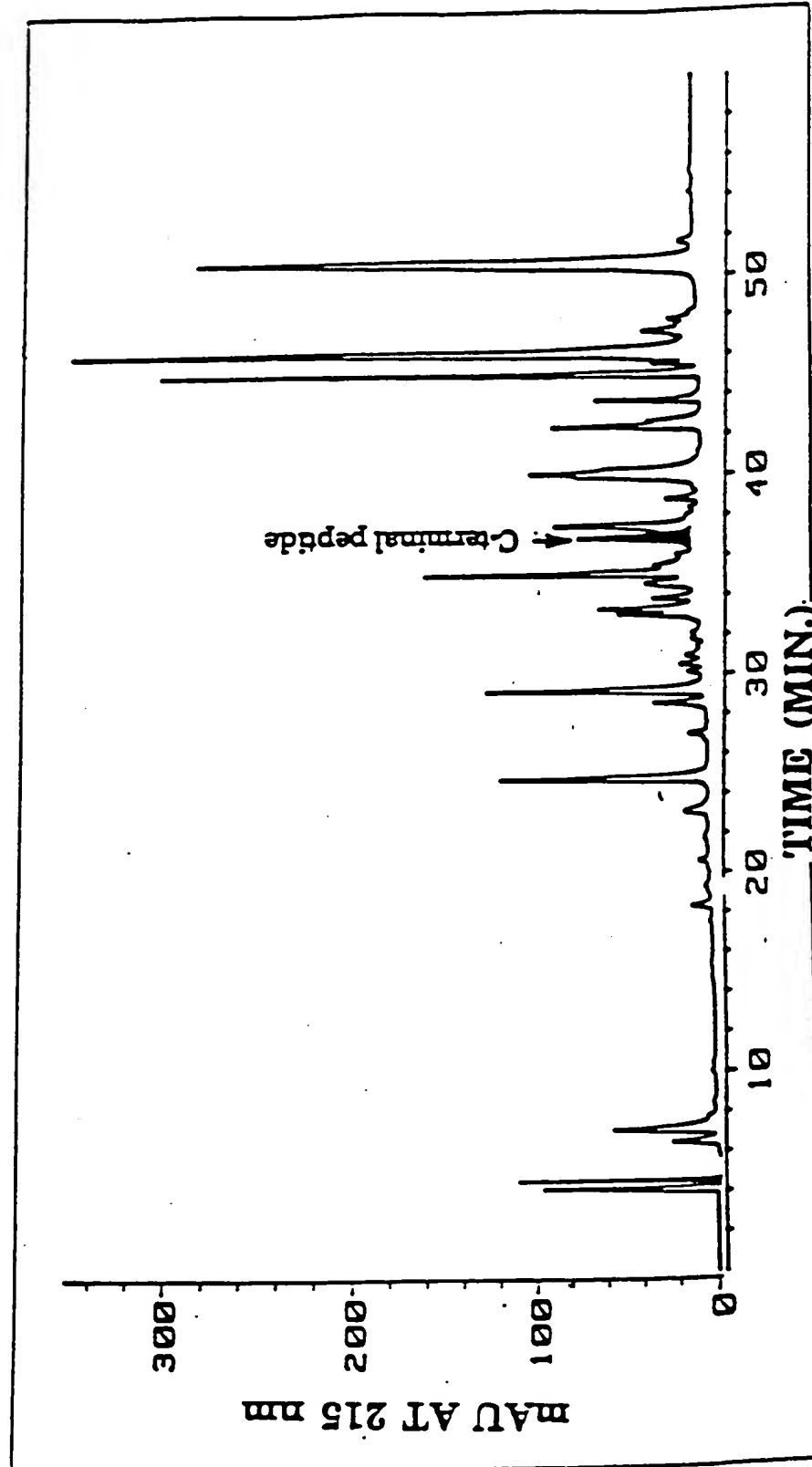


FIG. 16D

EcoRI

ta a t t taa t t c g t a
GAATTCCTTCGATATCTTCAACCGTTCCATCGACGCTTTCAAAGACTTCGTT
E F F R I F N R S I D A F K D F V

g a t tagt t t g t a at a ag t g
GTTGCTTCCGAAACCTCCGACTGCGTTGTTTCCTCCACCCTGTCTCCGGAA
V A S E T S D C V V S S T L S P E

BstEII

t a a cagt c a a t t a c t . a
AAAGACTCCCGTGTTTCGGTACCAAACCGTTTCATGCTGCCGCCGGTTGCT
K D S R V S V T K P F M L P P V A

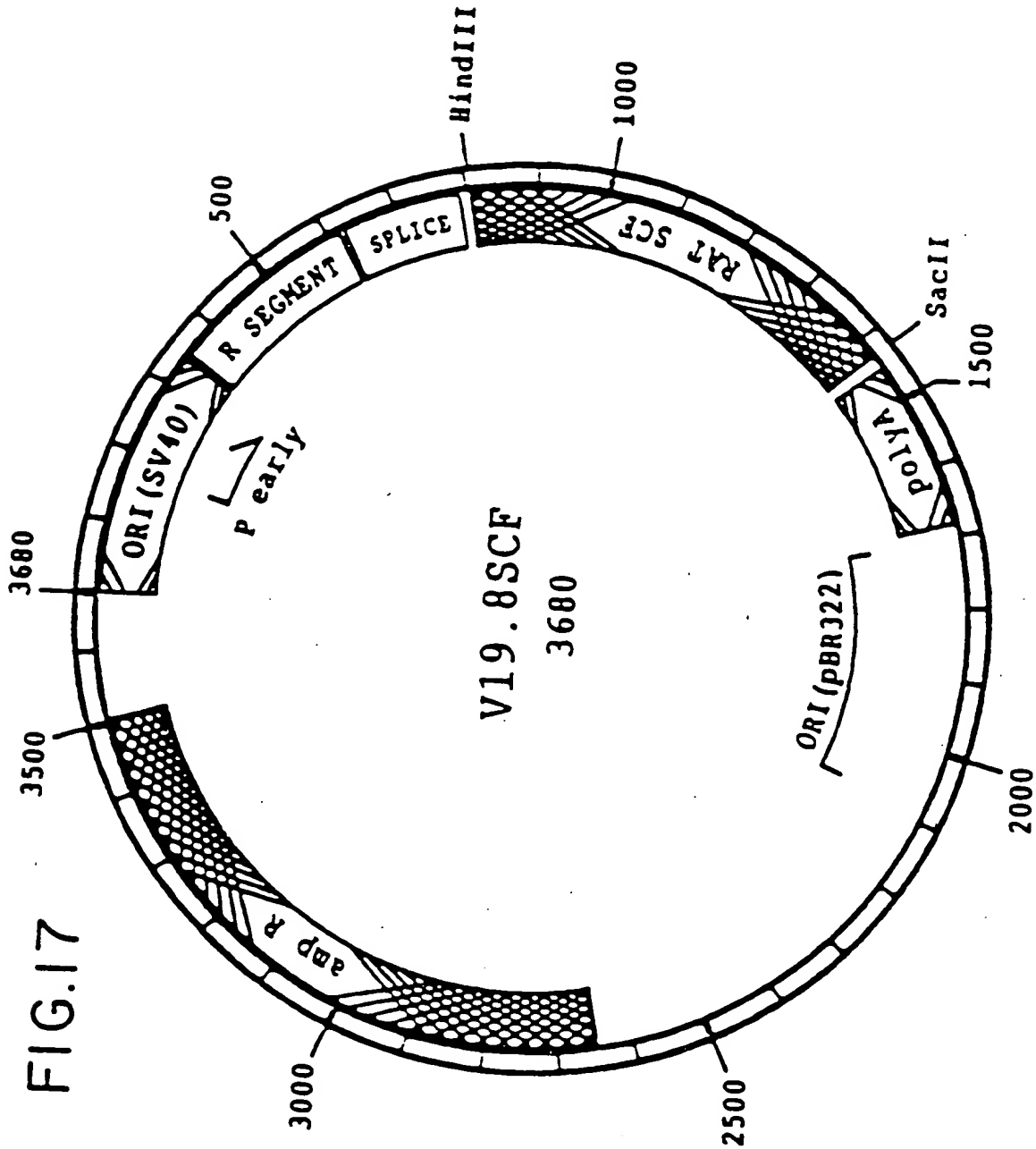
cag tag t ag agtag agt tagt g a t
GCTTCCTCCCTGCGTAACGACTCCTCCTCCTCCAACCTCCAAATACATCTAC
A S S L R N D S S S S N S K Y I Y

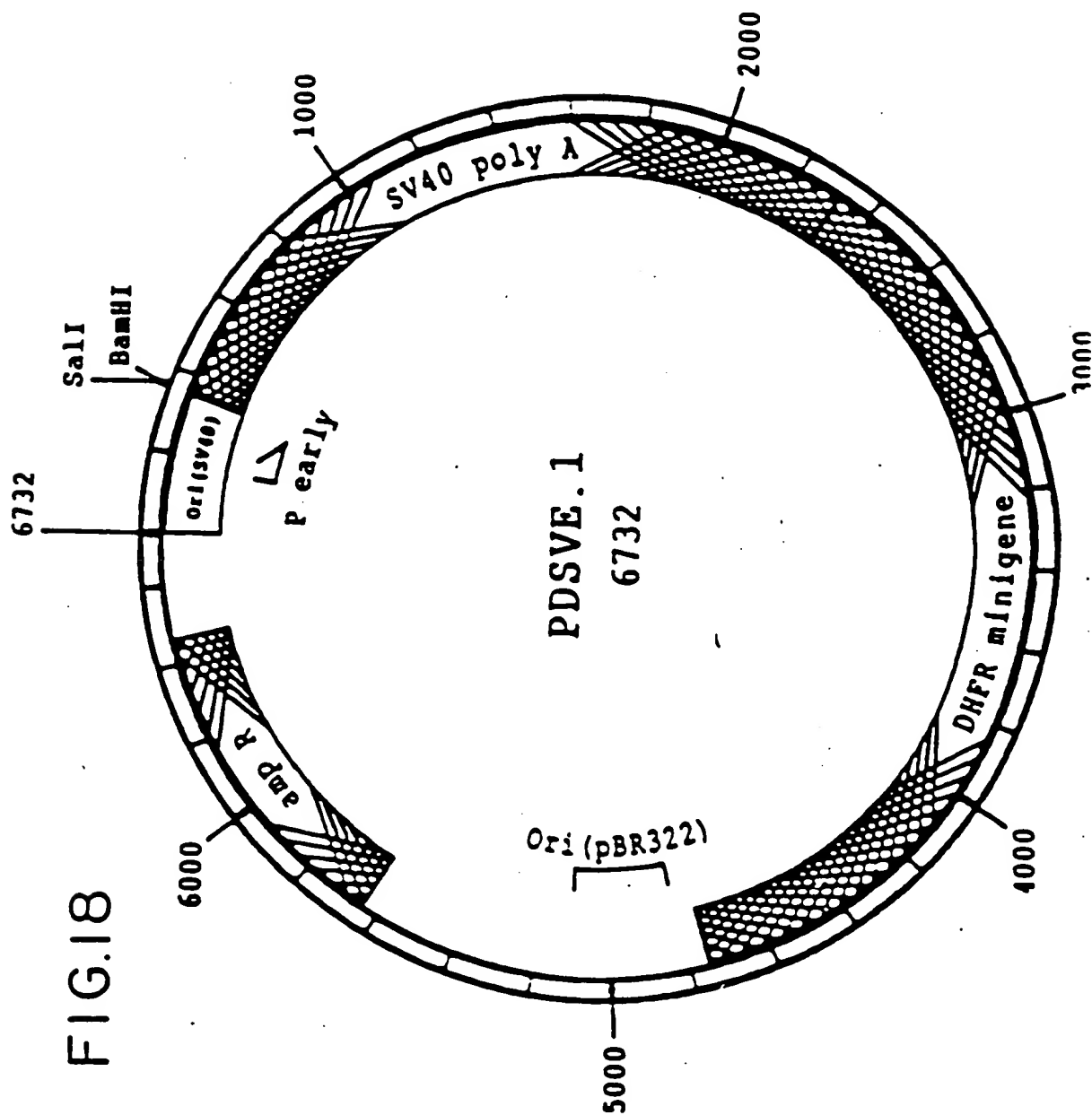
BamHI

t
CTGATCTAATAGGATCC
L I . .

FIG. 16E

BstEII
GGTTACCAAACCGTTCATGCTGCCGCCGGTTGCTGCTTAATAGGATCC BamHI
V T K P F M L P P V A A . .





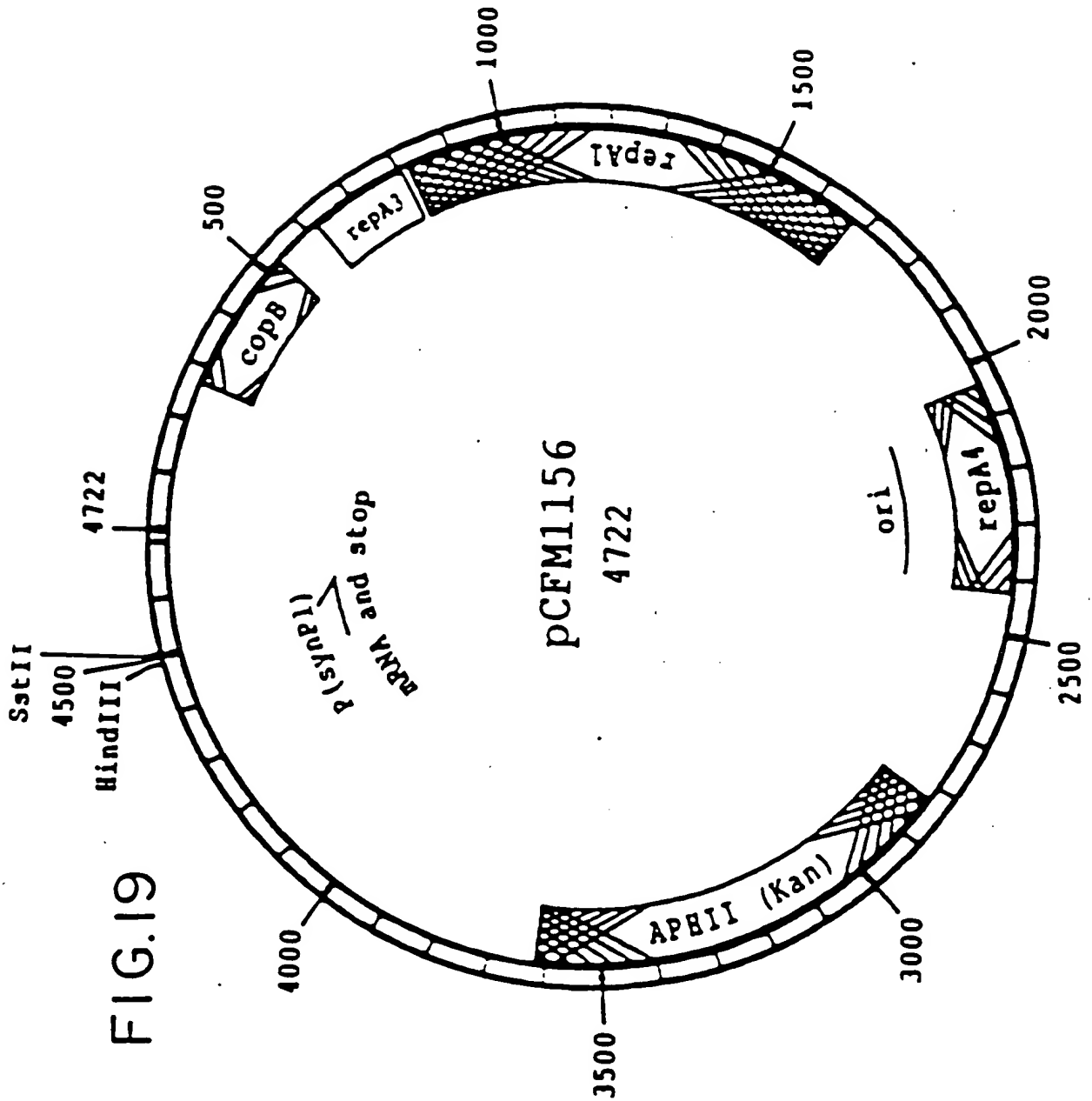


FIG. 20A

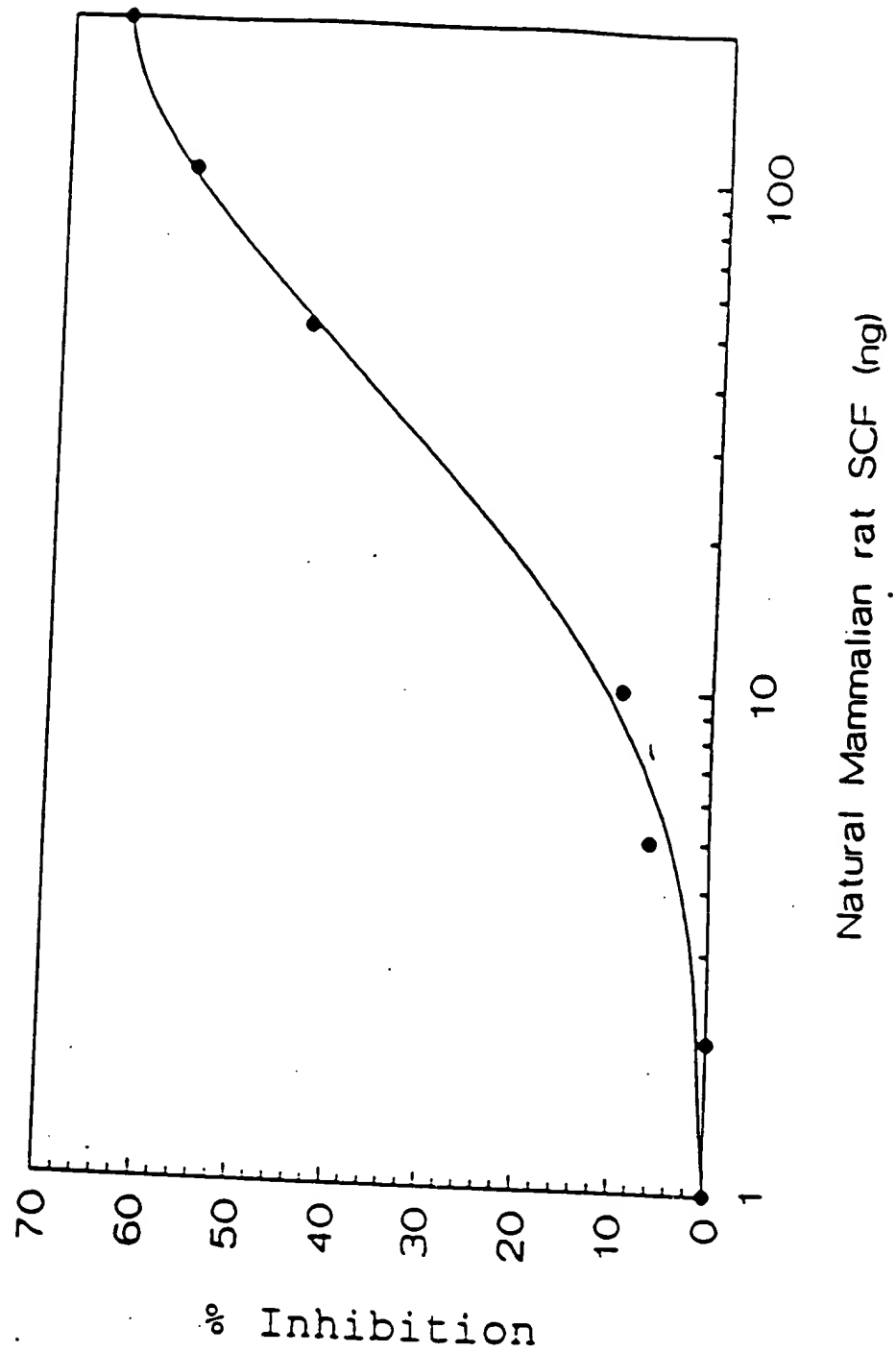


FIG. 20B

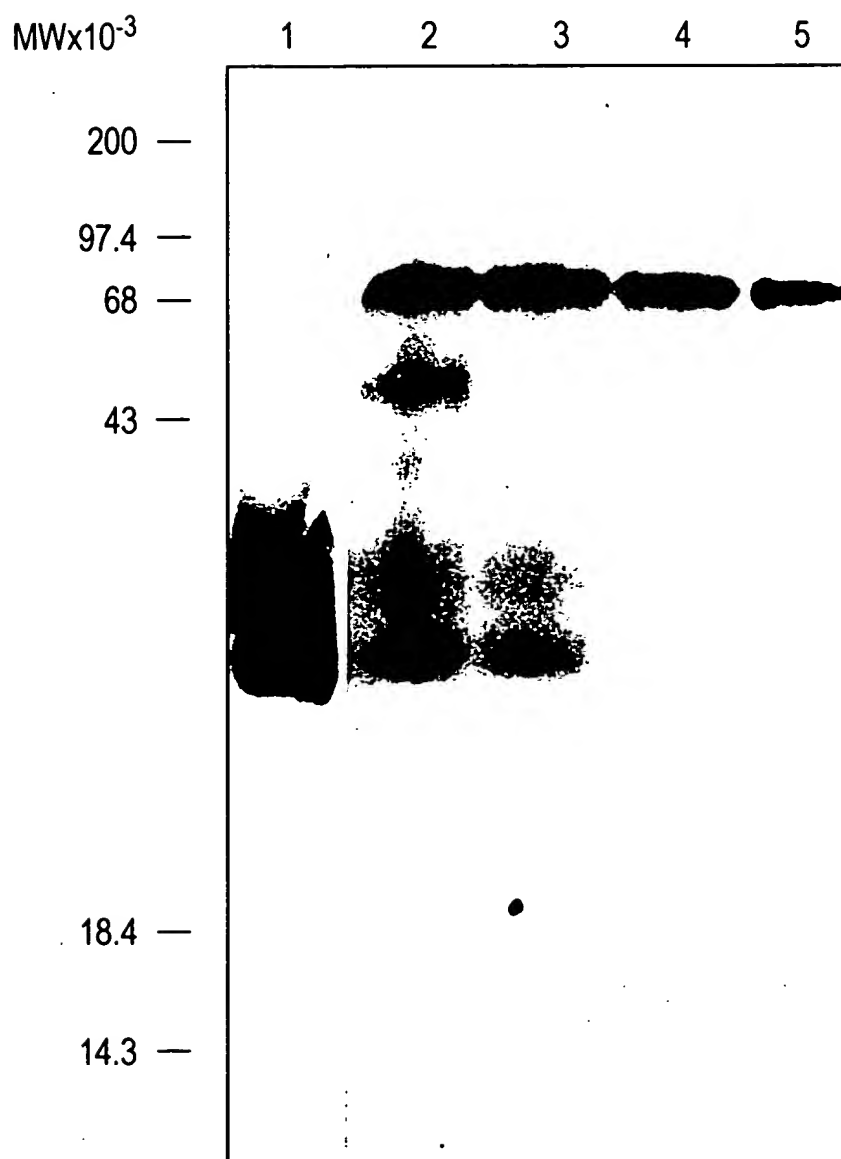
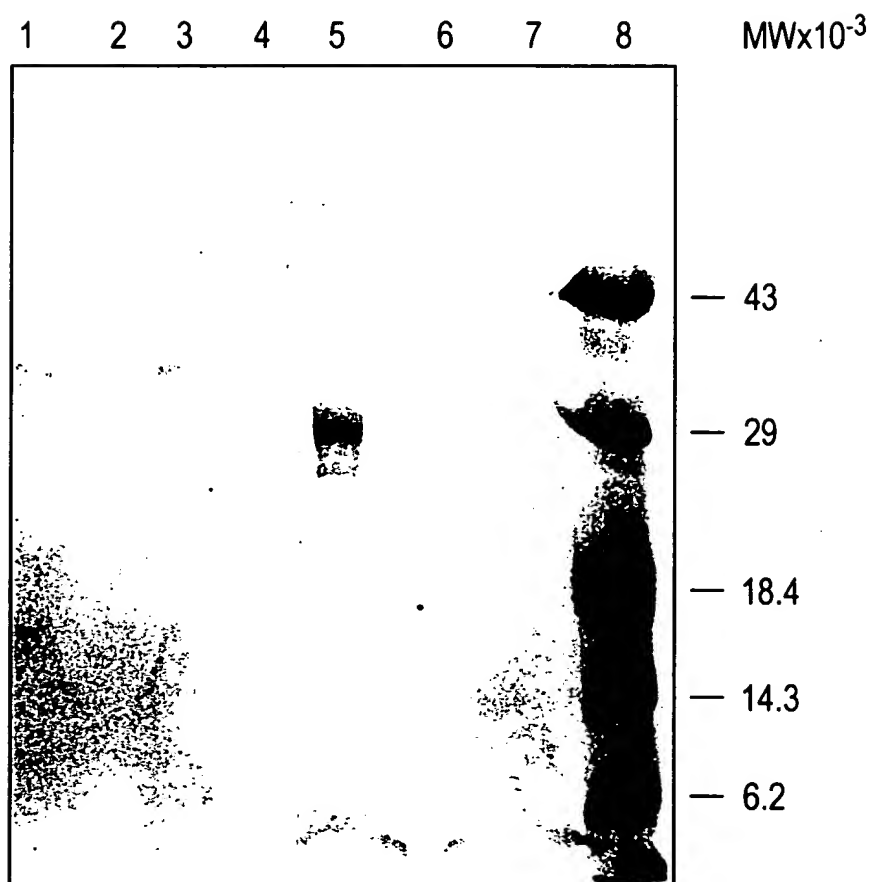


FIG. 21



The figure is a GPC chromatogram with two traces. The x-axis is labeled 'ml' and ranges from 1 to 10. The y-axis is labeled 'MW x 10⁻³' and has tick marks at 14.3, 18.4, 29, 43, 68, 97.4, and 200. The top trace, labeled 'P2VP', shows a broad peak centered around 6.5 ml. The bottom trace, labeled 'P2VP-co-PVCz', shows a much narrower peak centered around 6.5 ml. Both traces have a baseline that rises sharply after 6 ml and then levels off.

FIG. 22A

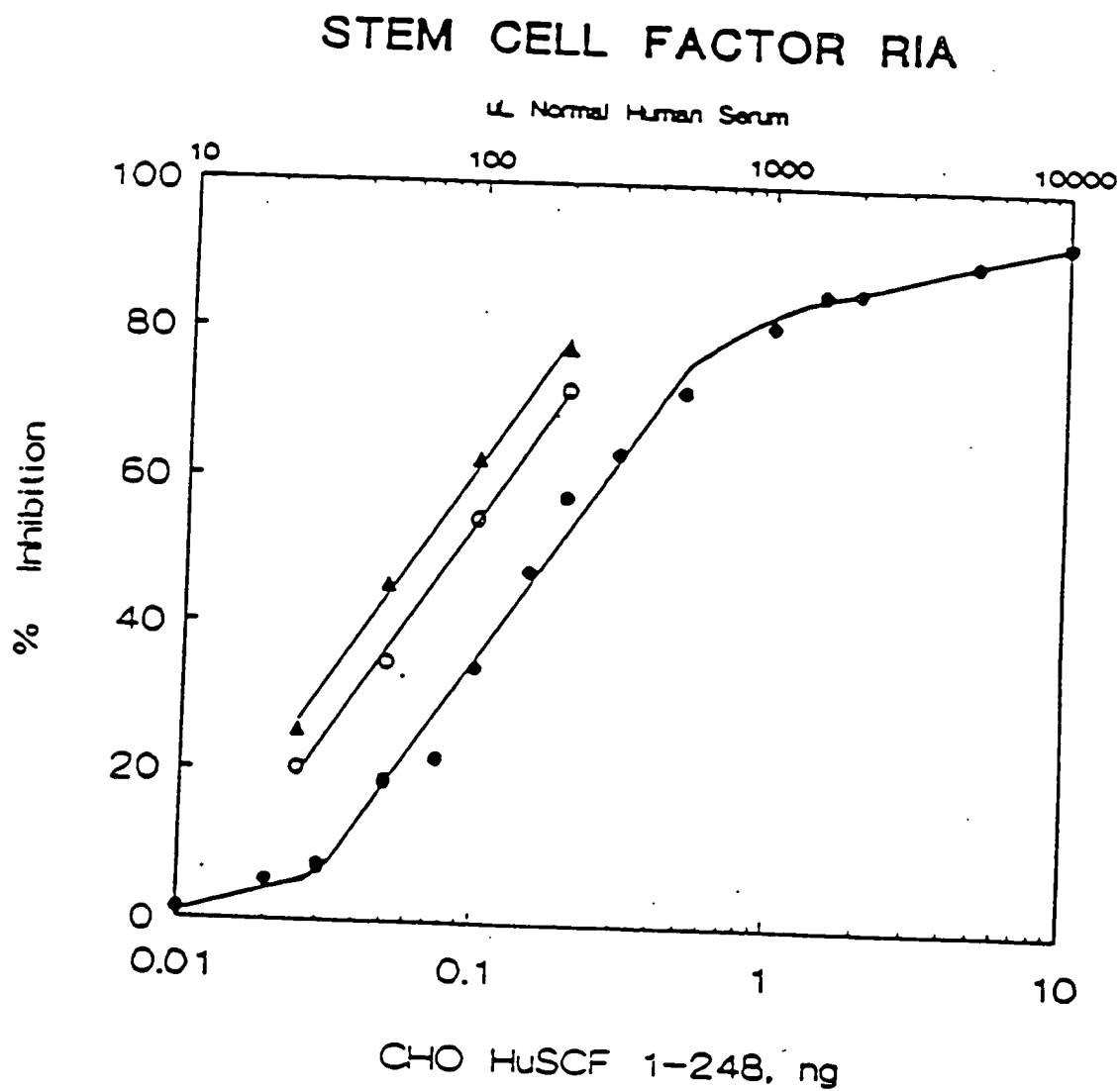
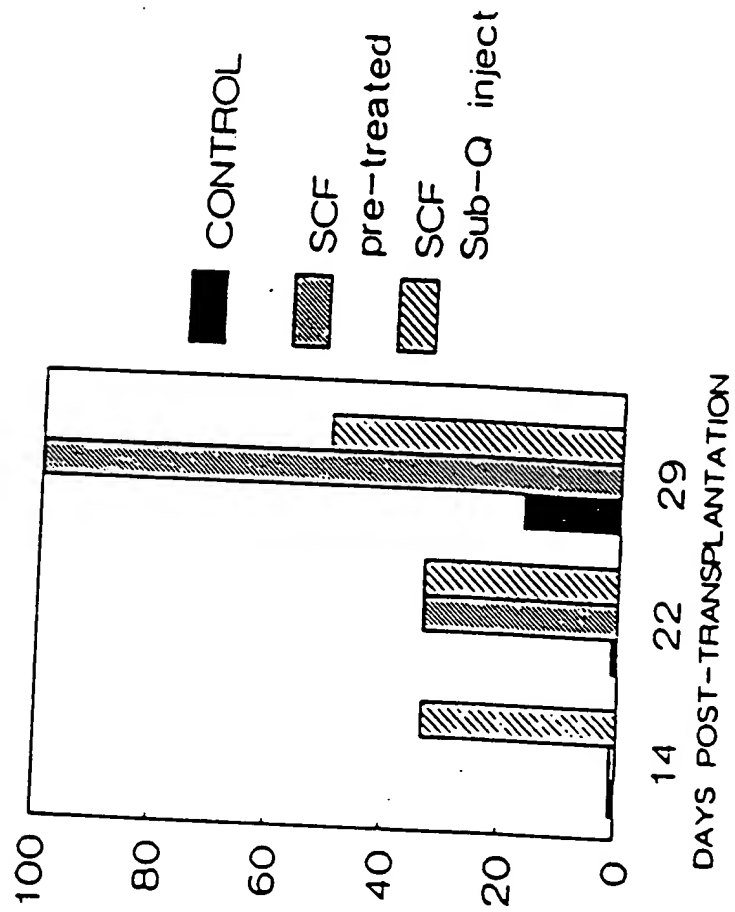


FIG. 23



* MICE CONVERTED TO DONOR PHENOTYPE

FIG. 24A

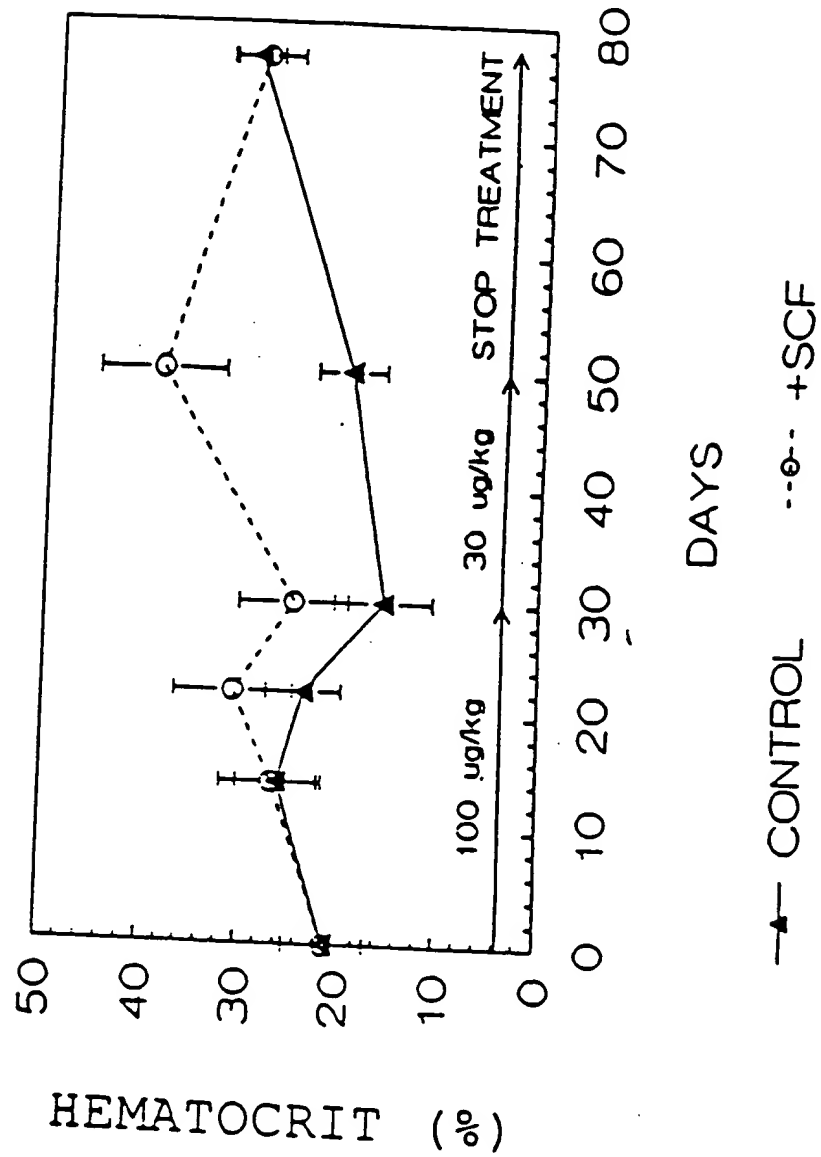


FIG. 24B

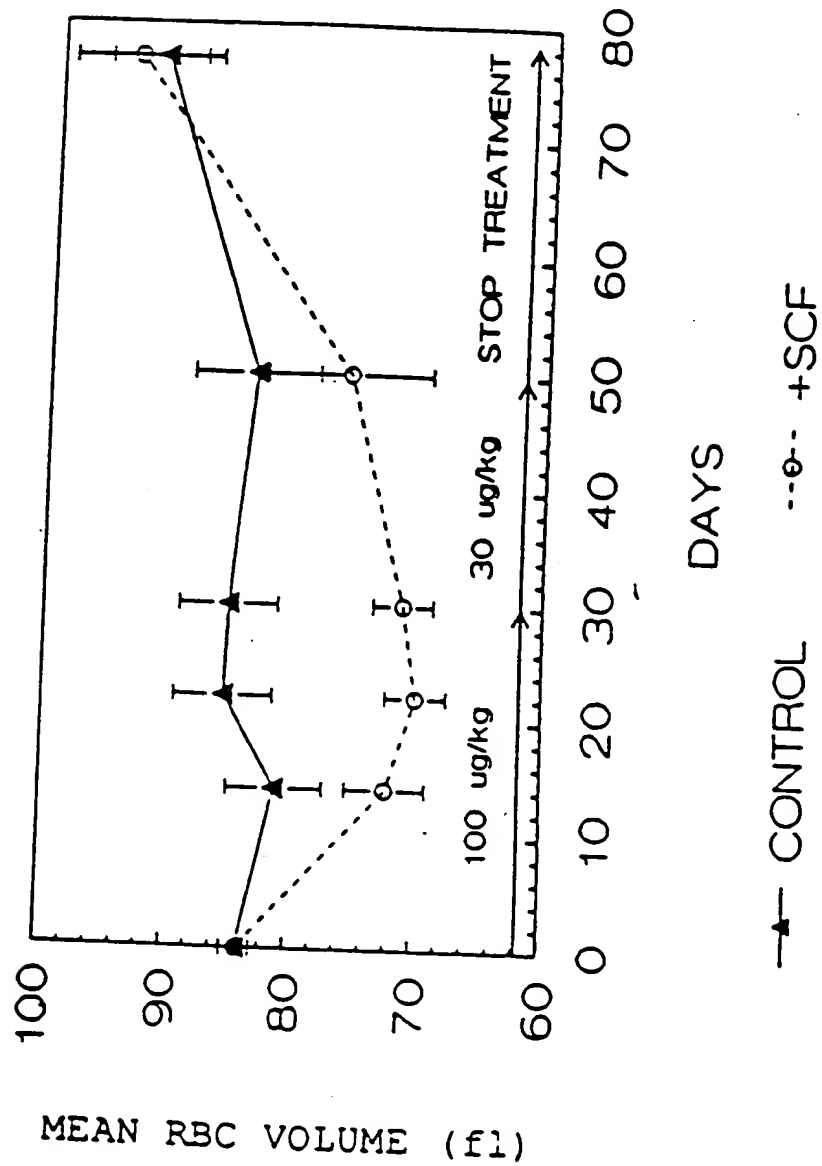


FIG. 25

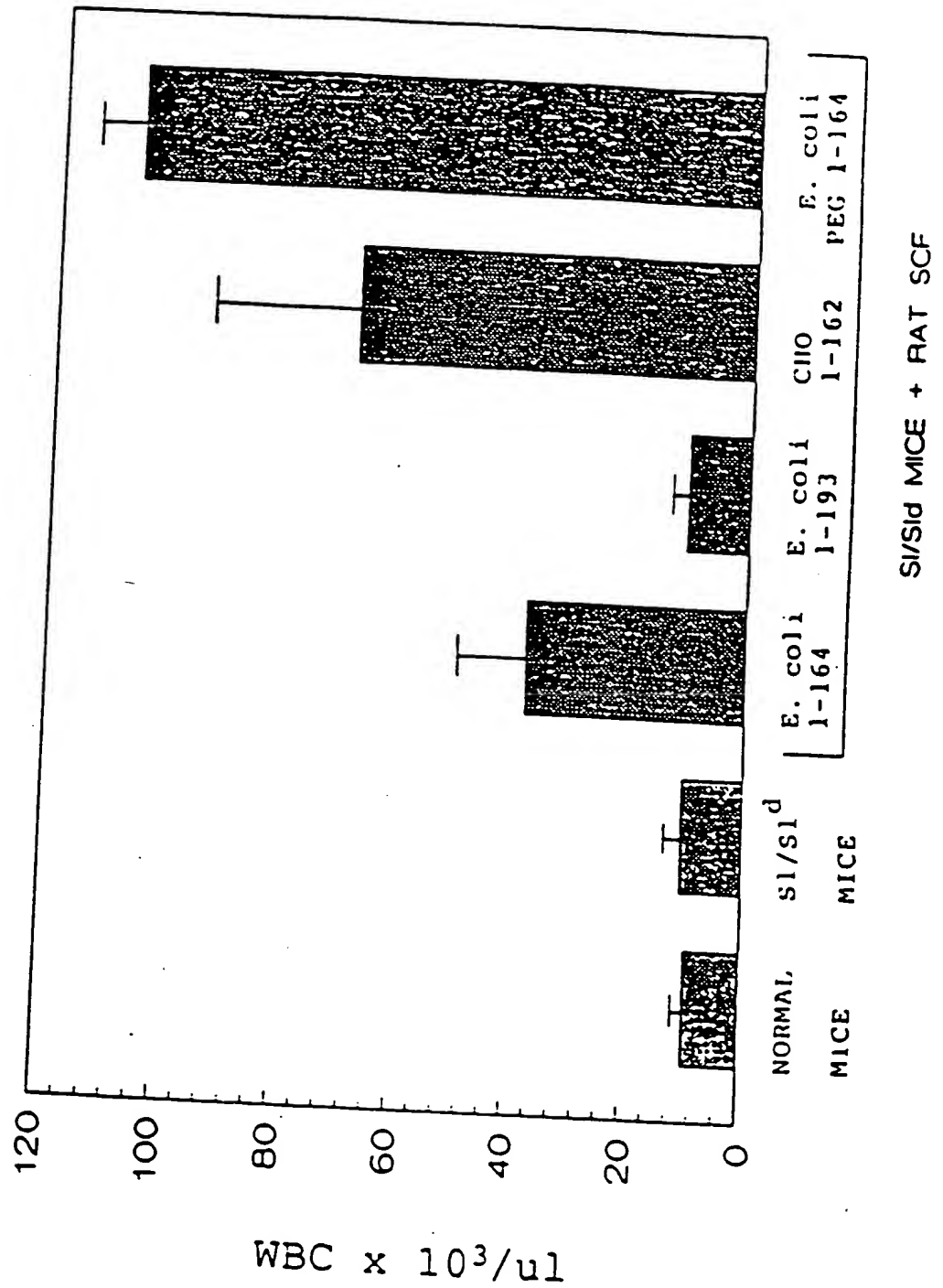


FIG. 26

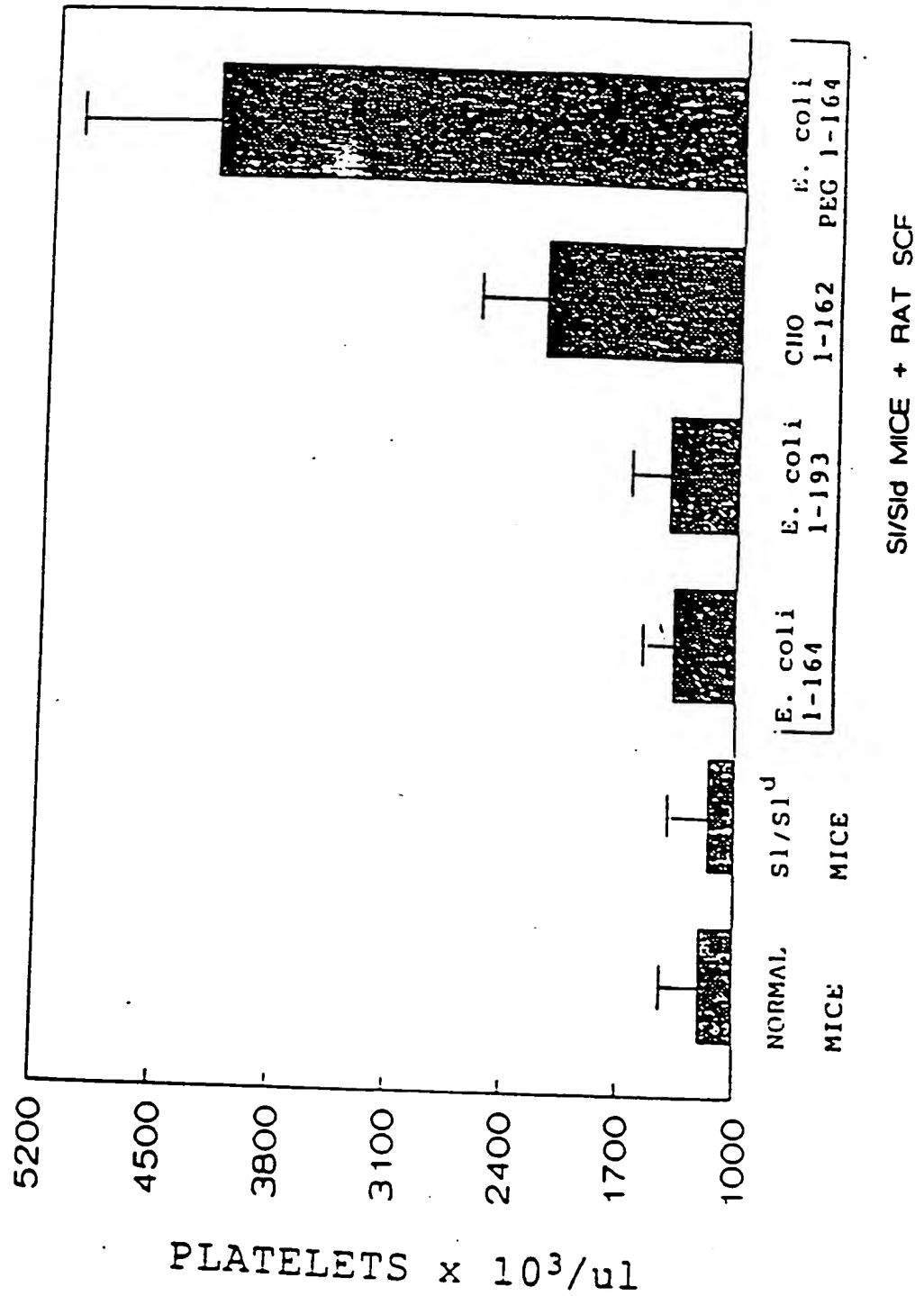


FIG. 27

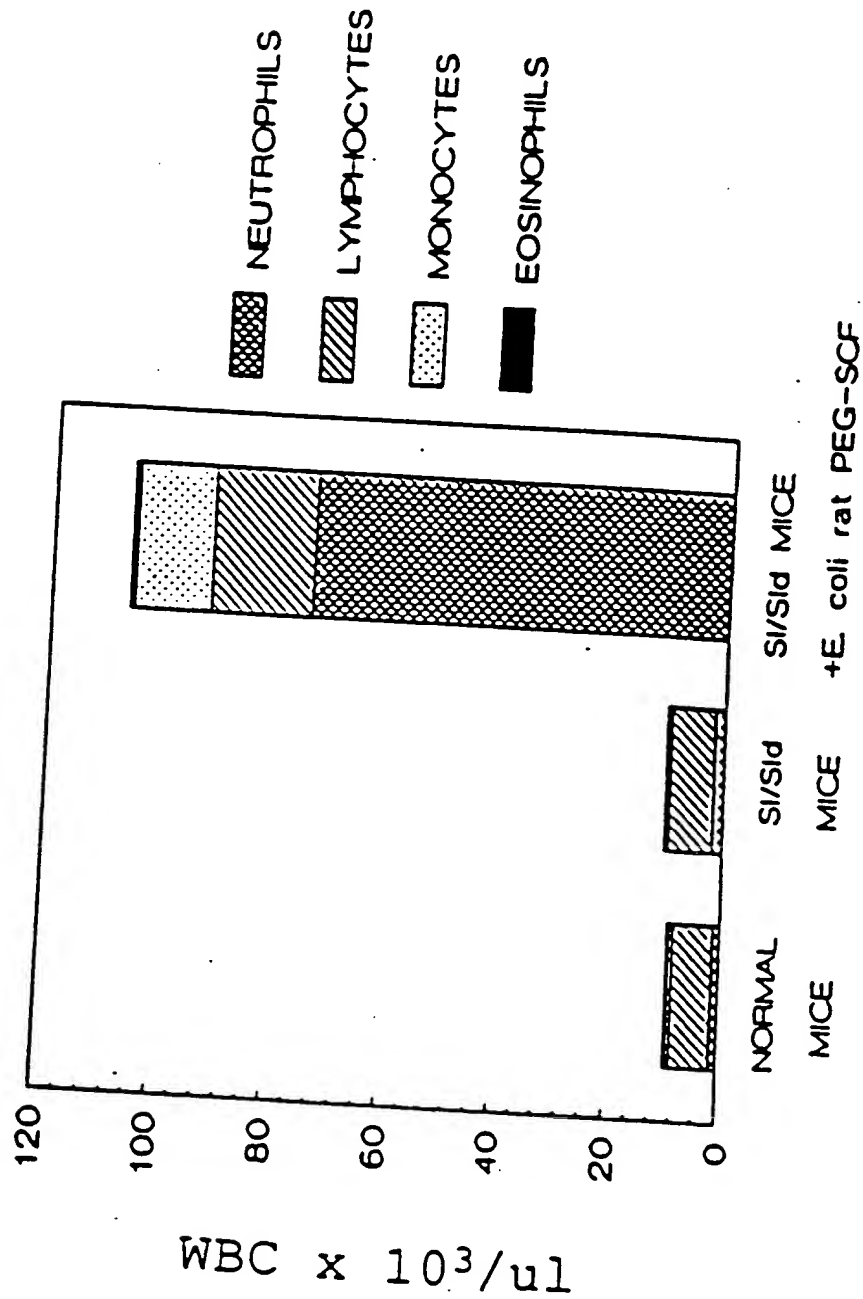


FIG. 28

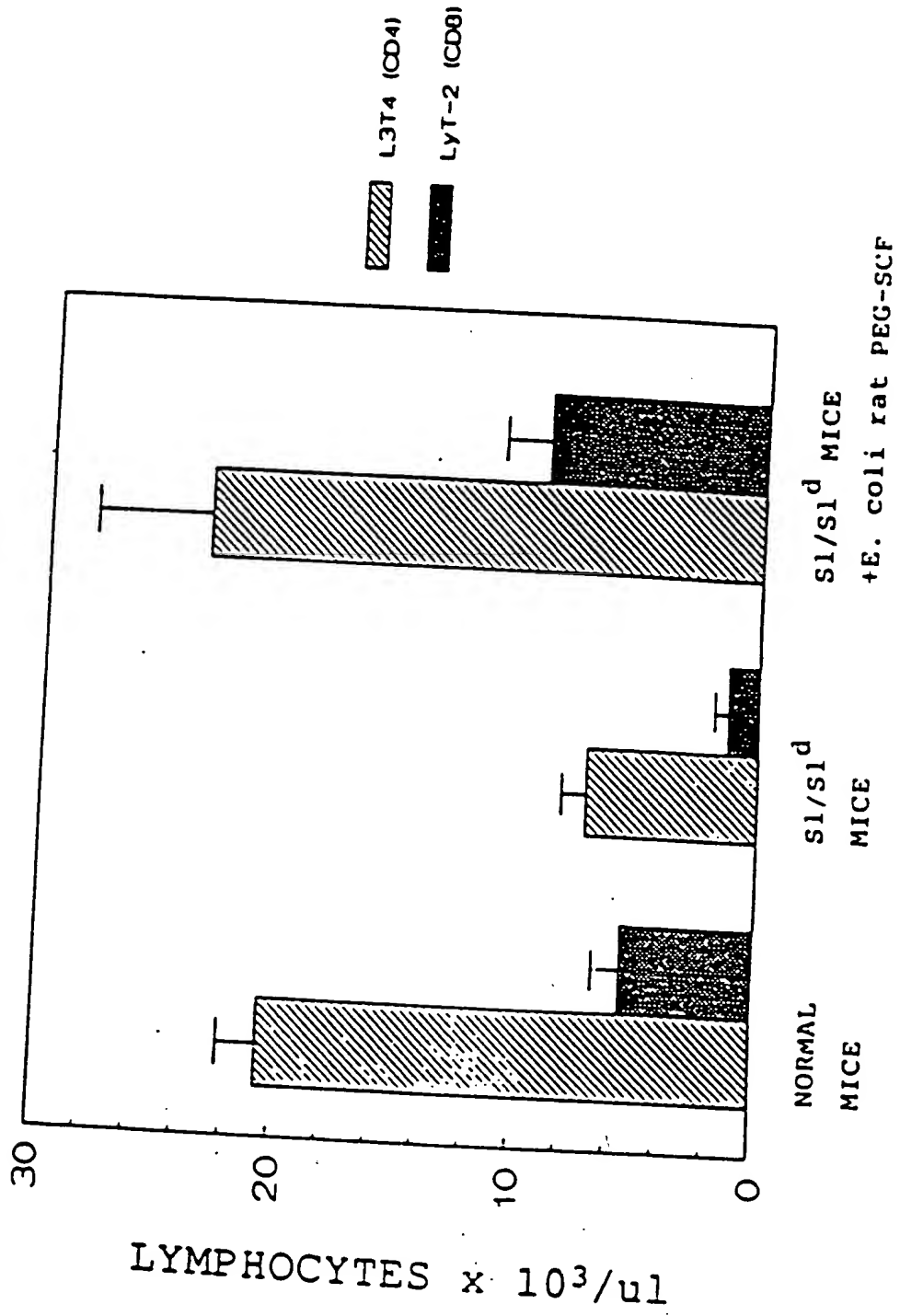
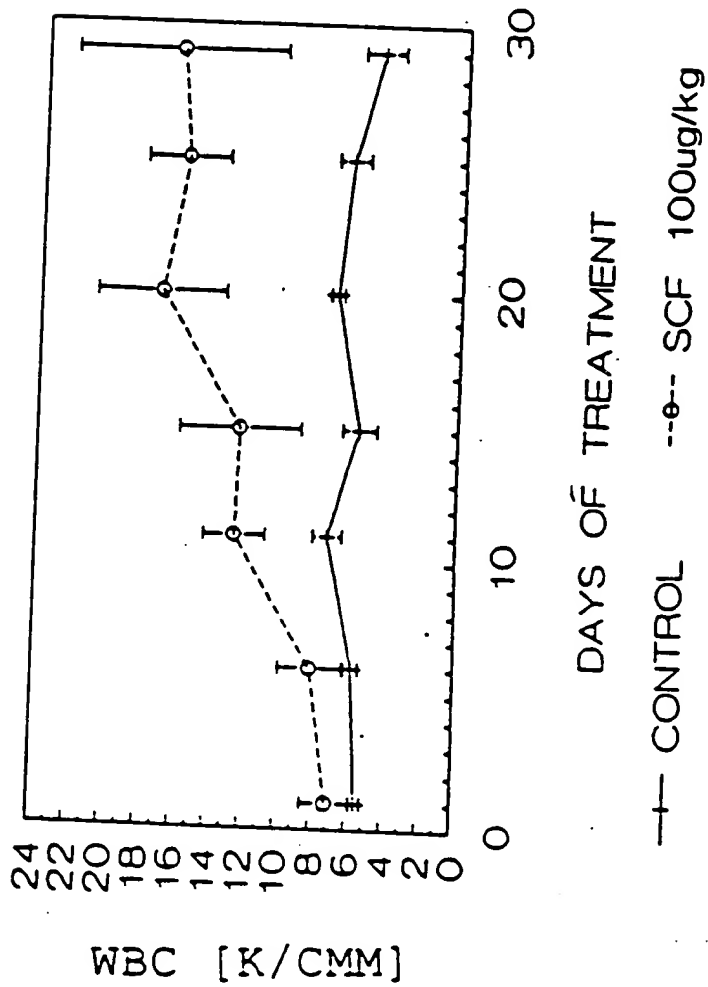
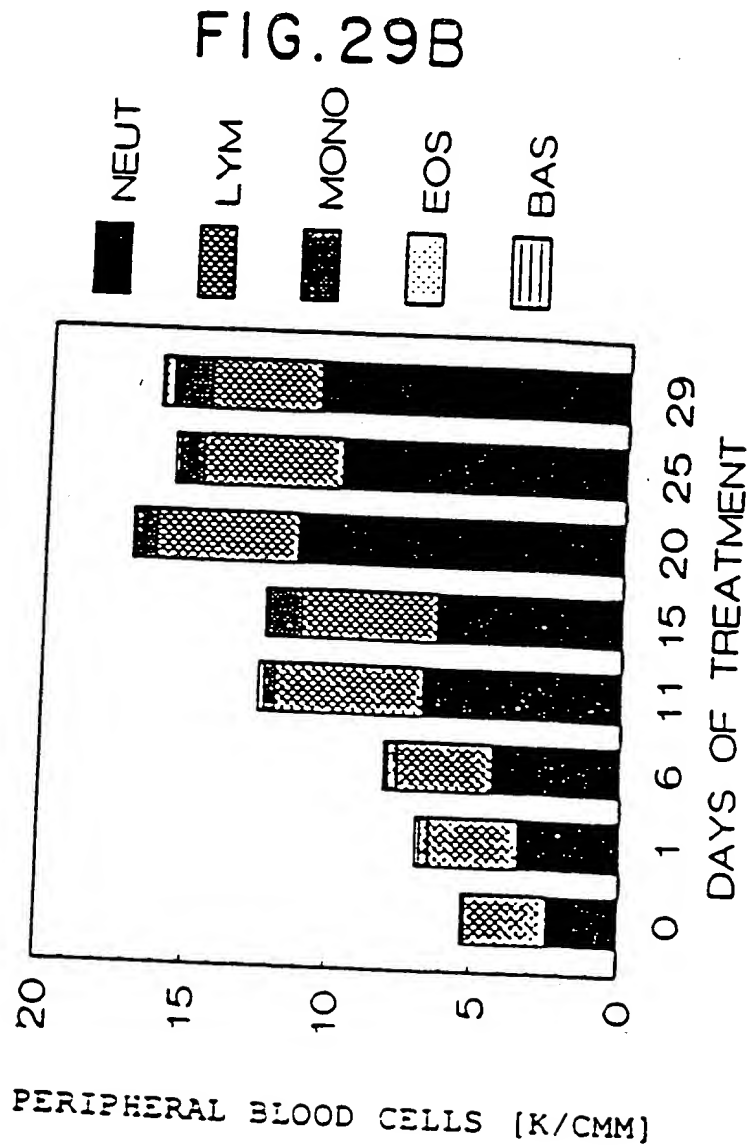


FIG. 29A





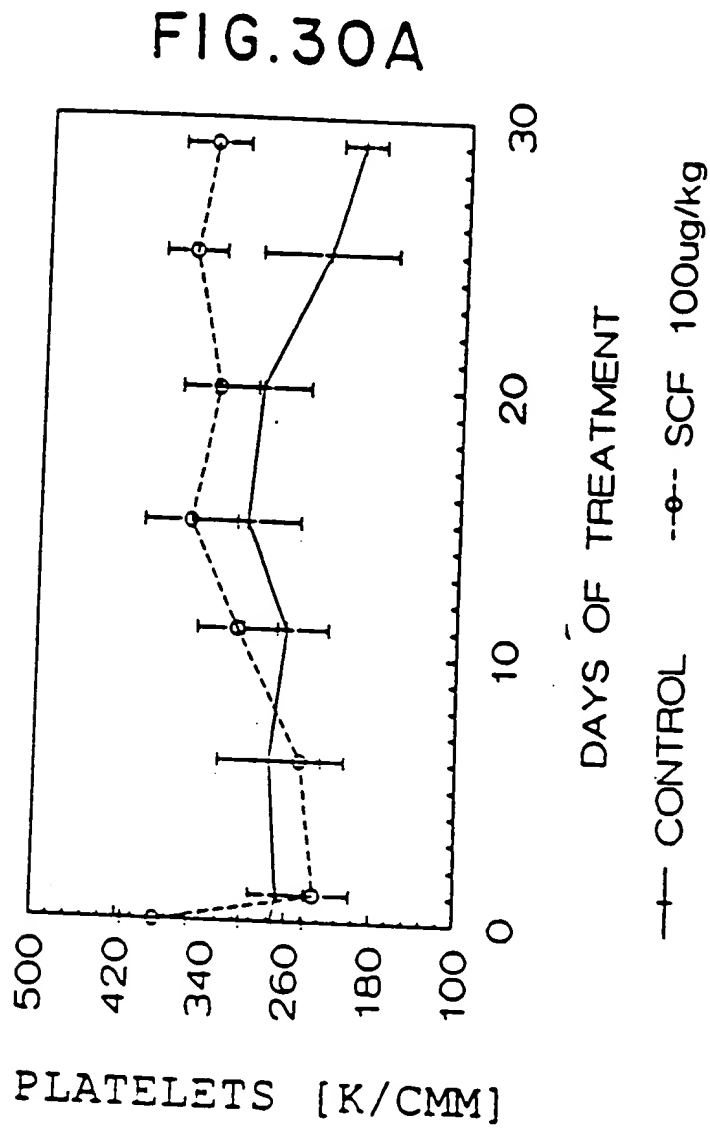


FIG. 30B

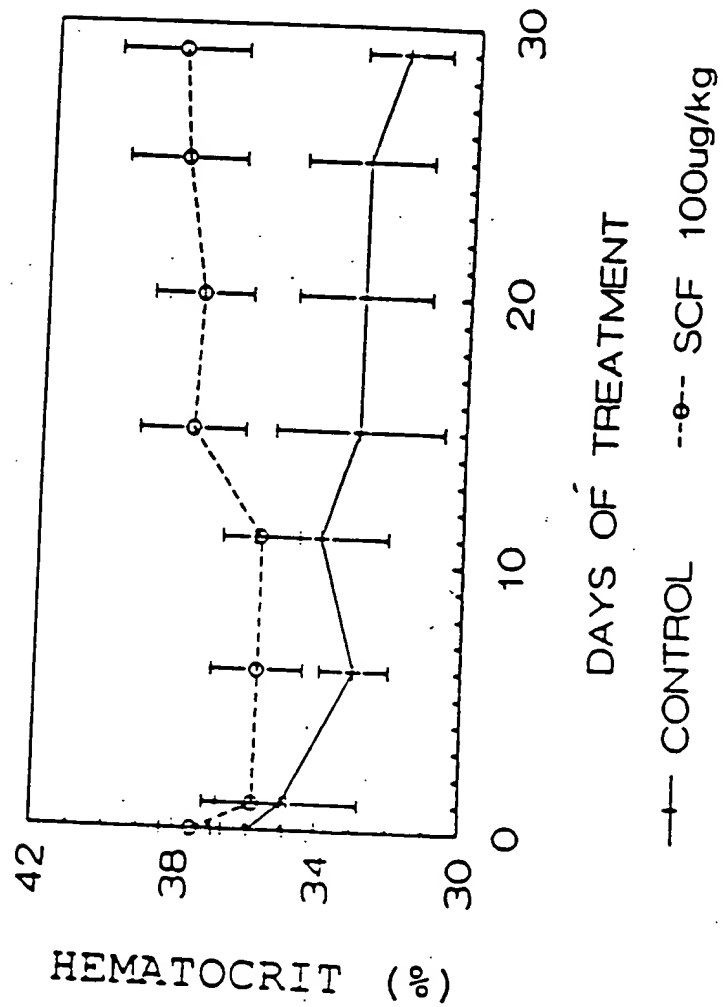


FIG. 31B

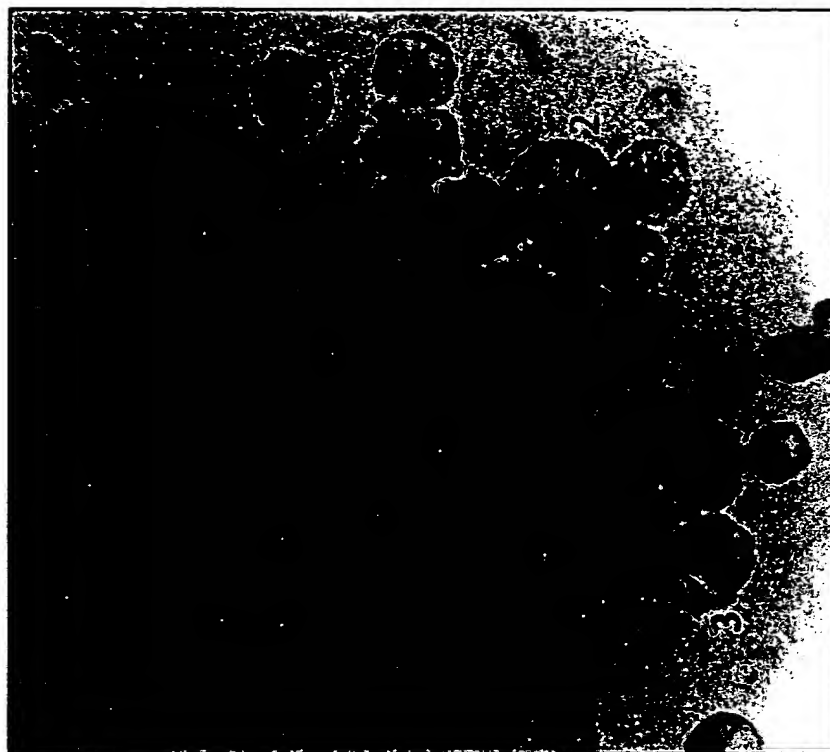


FIG. 31A

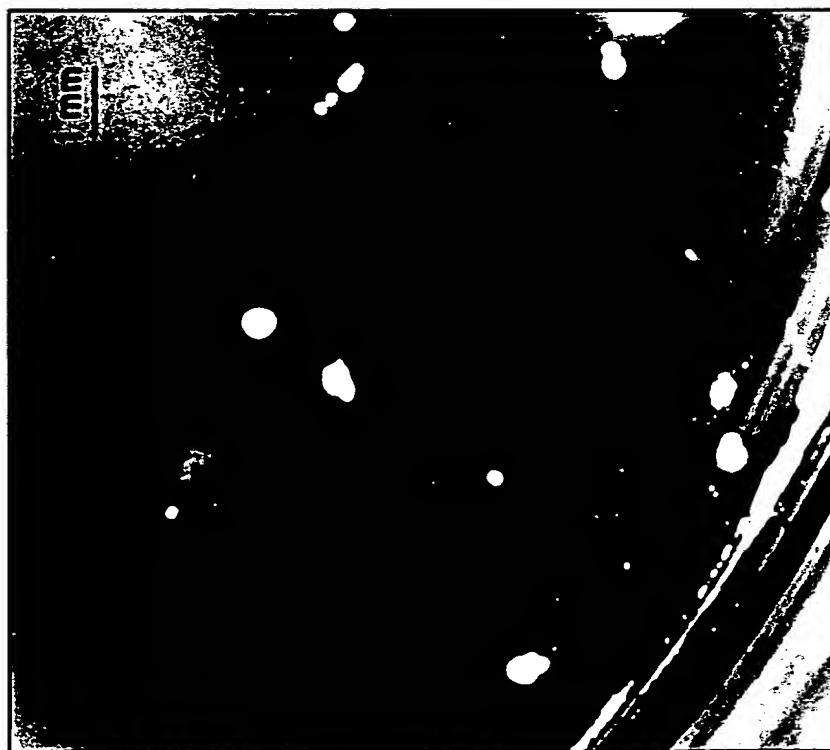


FIG. 31C

SCF4 SMP4

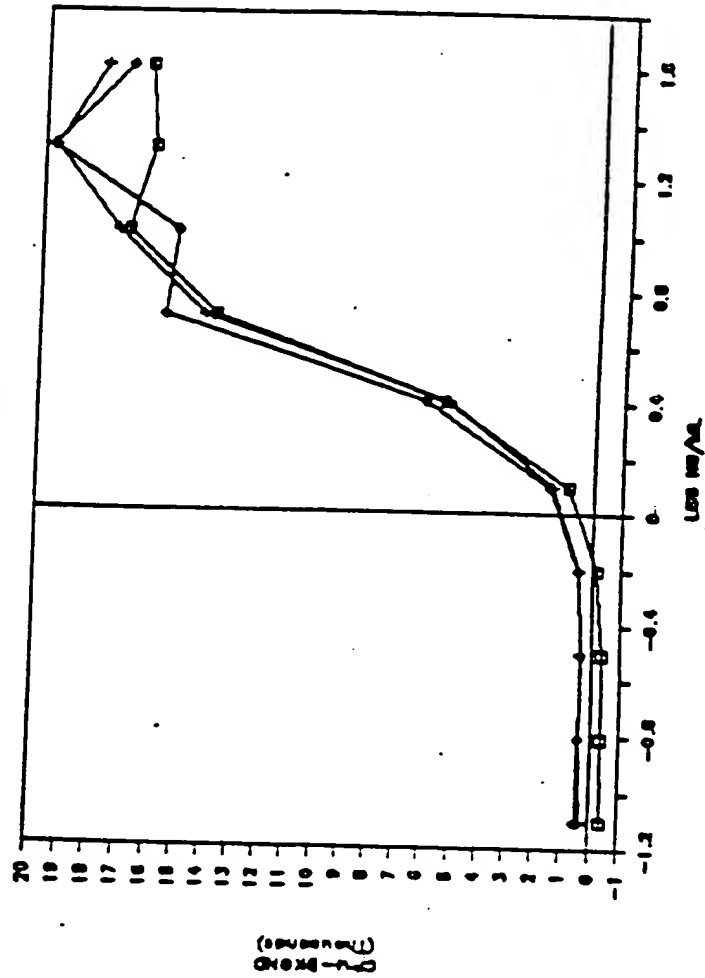
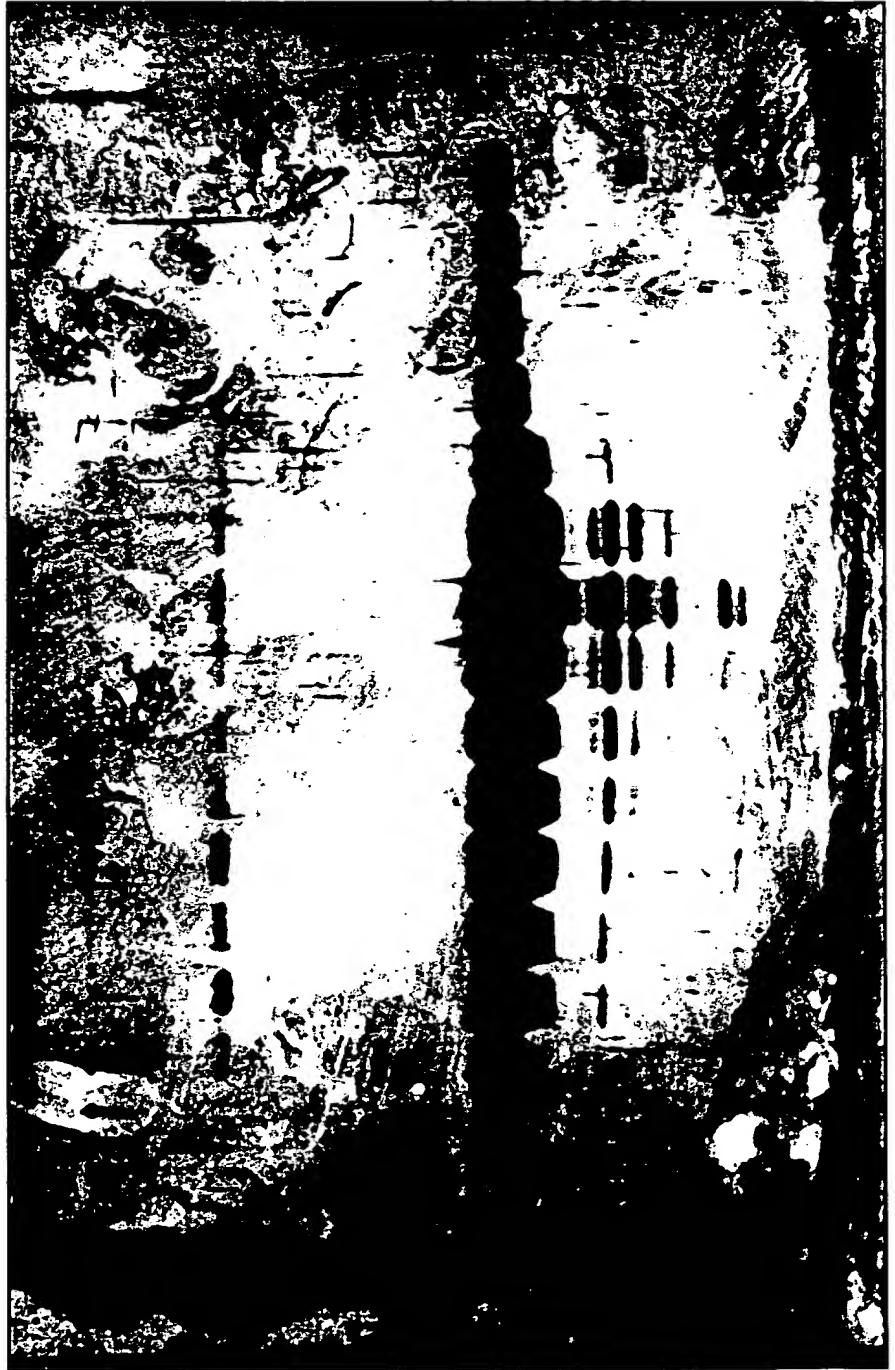


FIG. 32A

S Sepharose Load

37
35
33
31
29
27
25
23
21
19
17
15
13
11



97.4 —
66.2 —
42.7 —
31.1 —
21.5 —
14.4 —

FIG. 32B

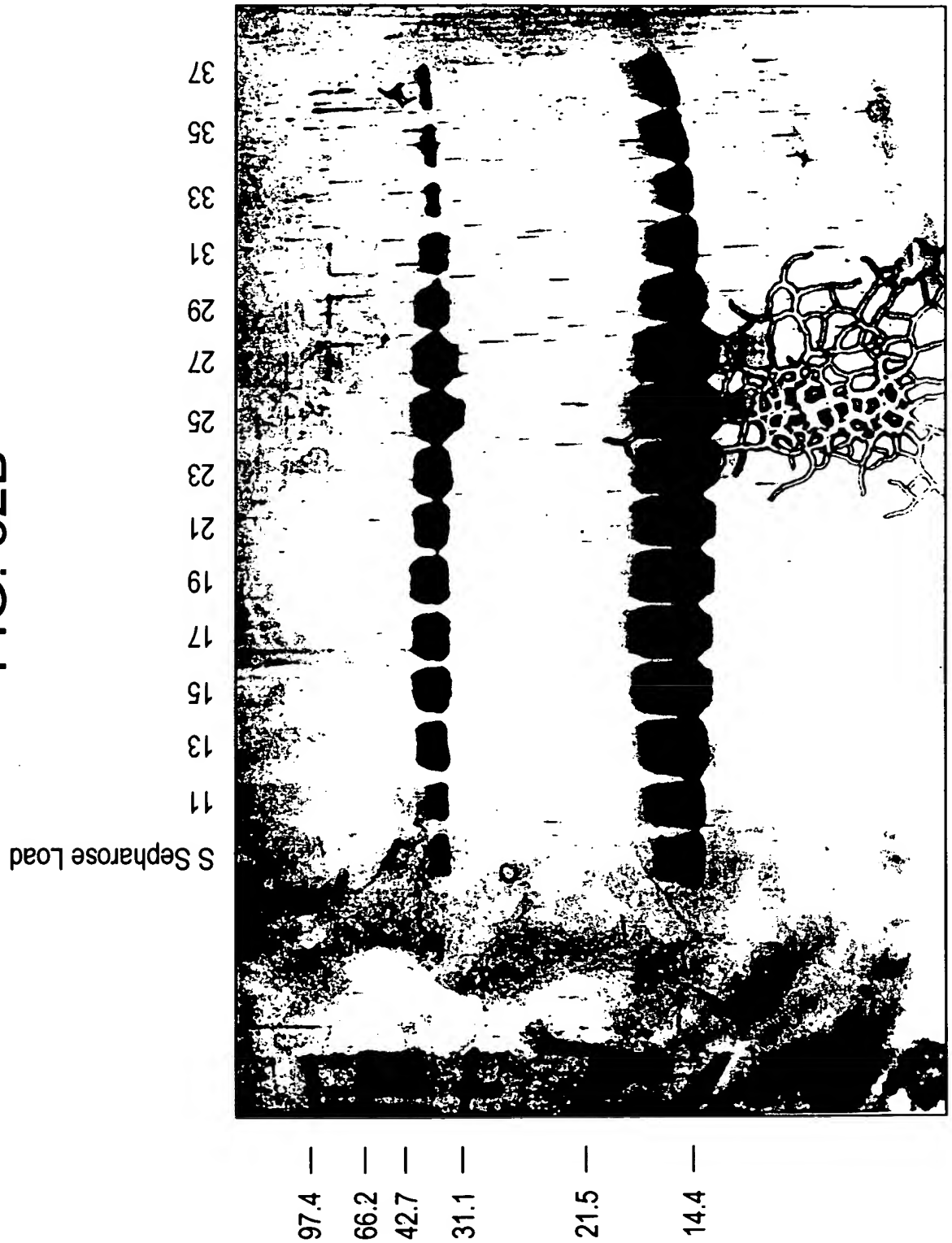


FIG. 33

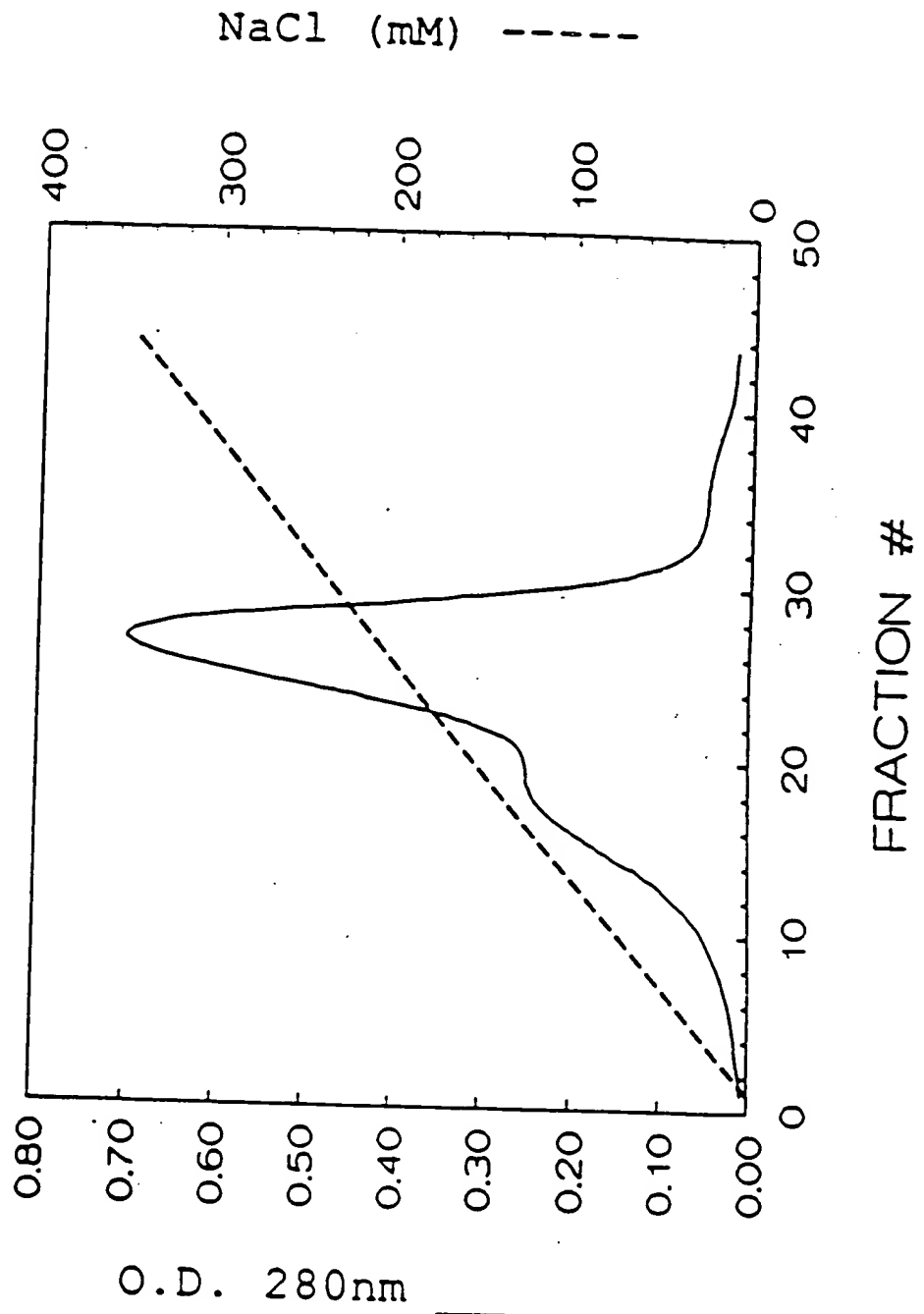
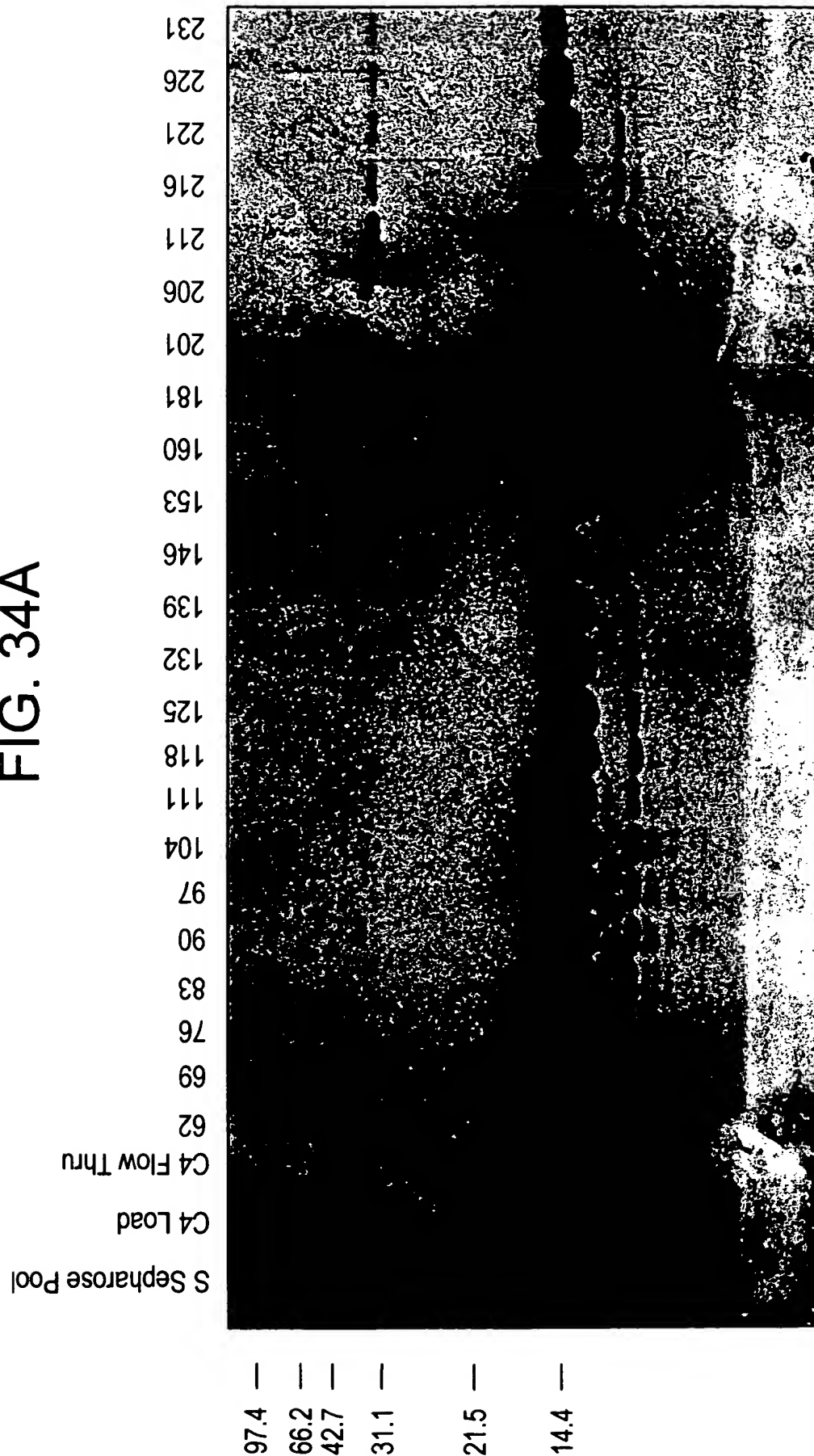
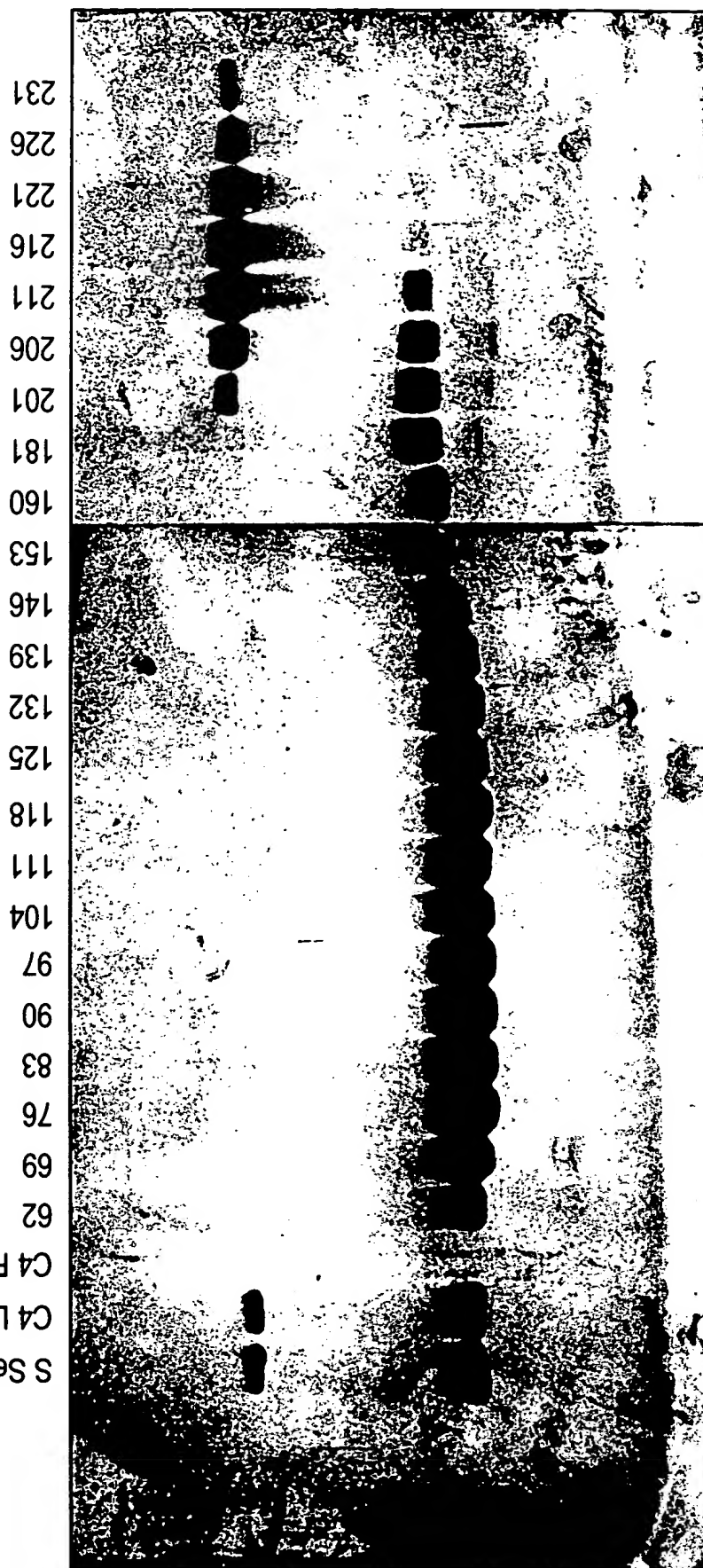
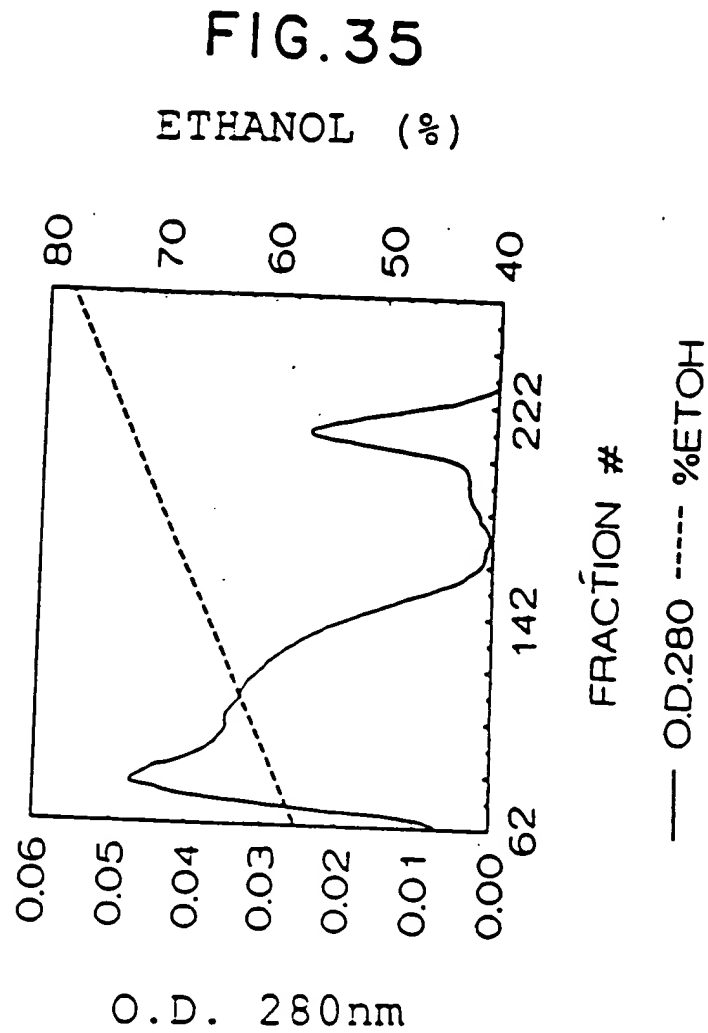
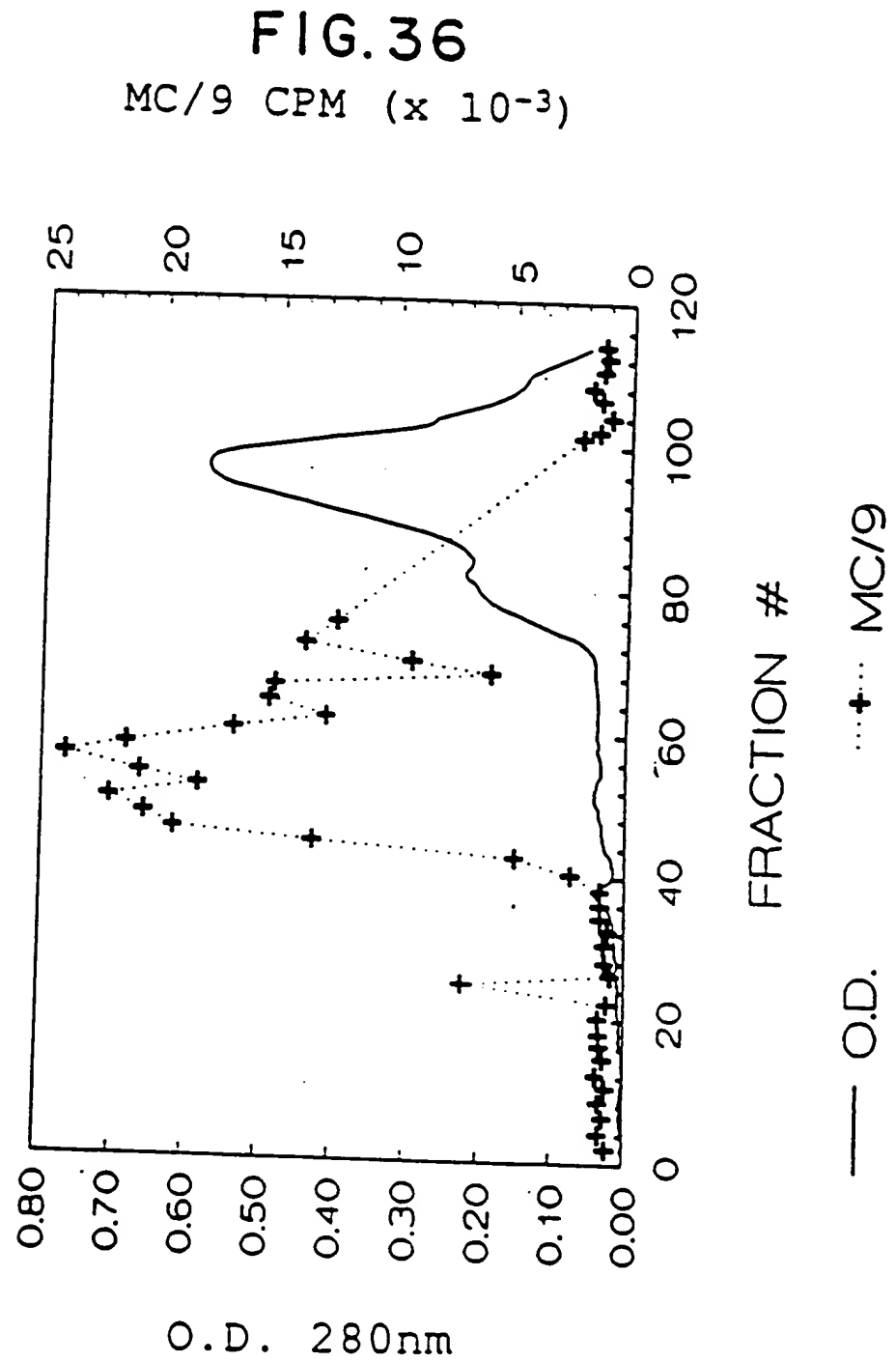


FIG. 34A









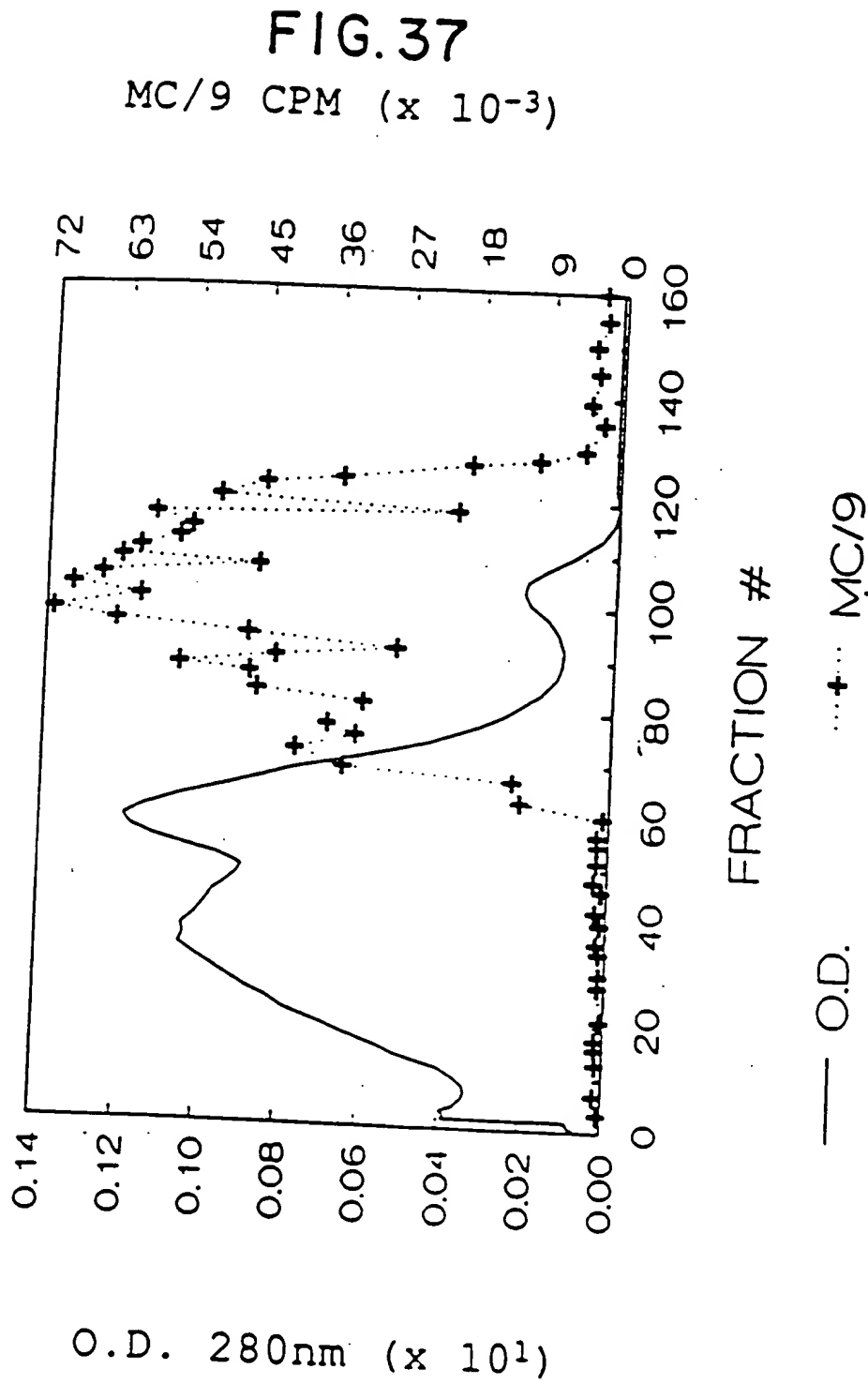
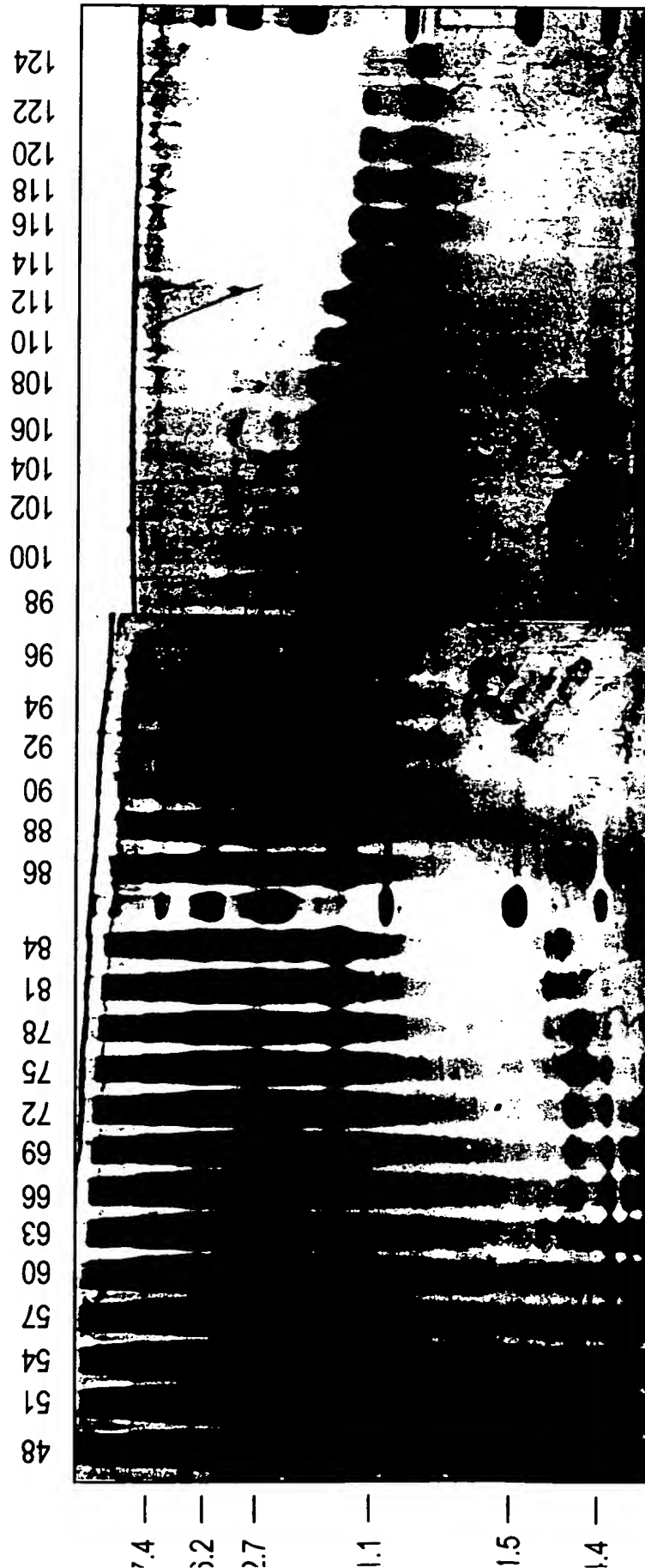


FIG. 38



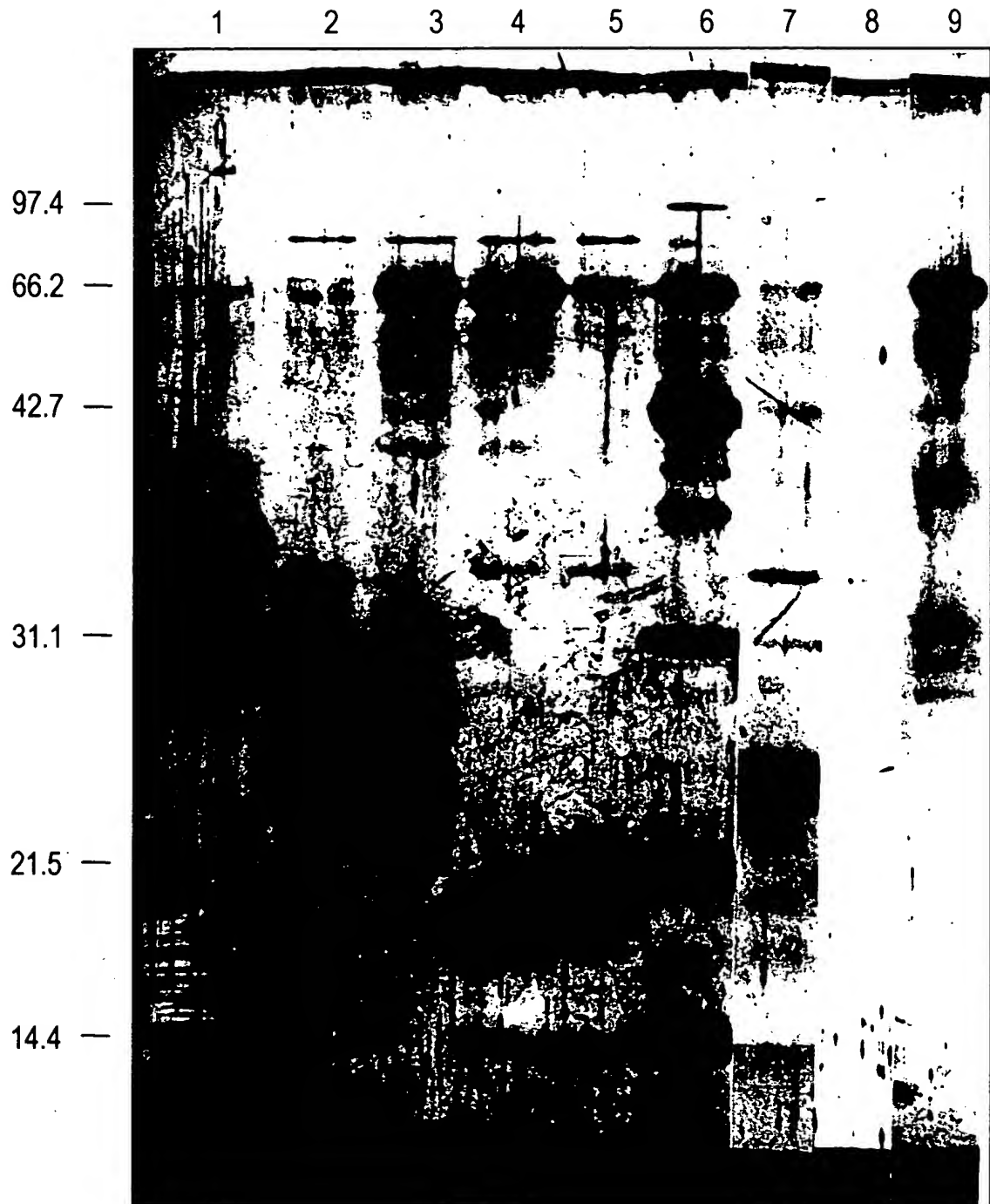


FIG. 40A

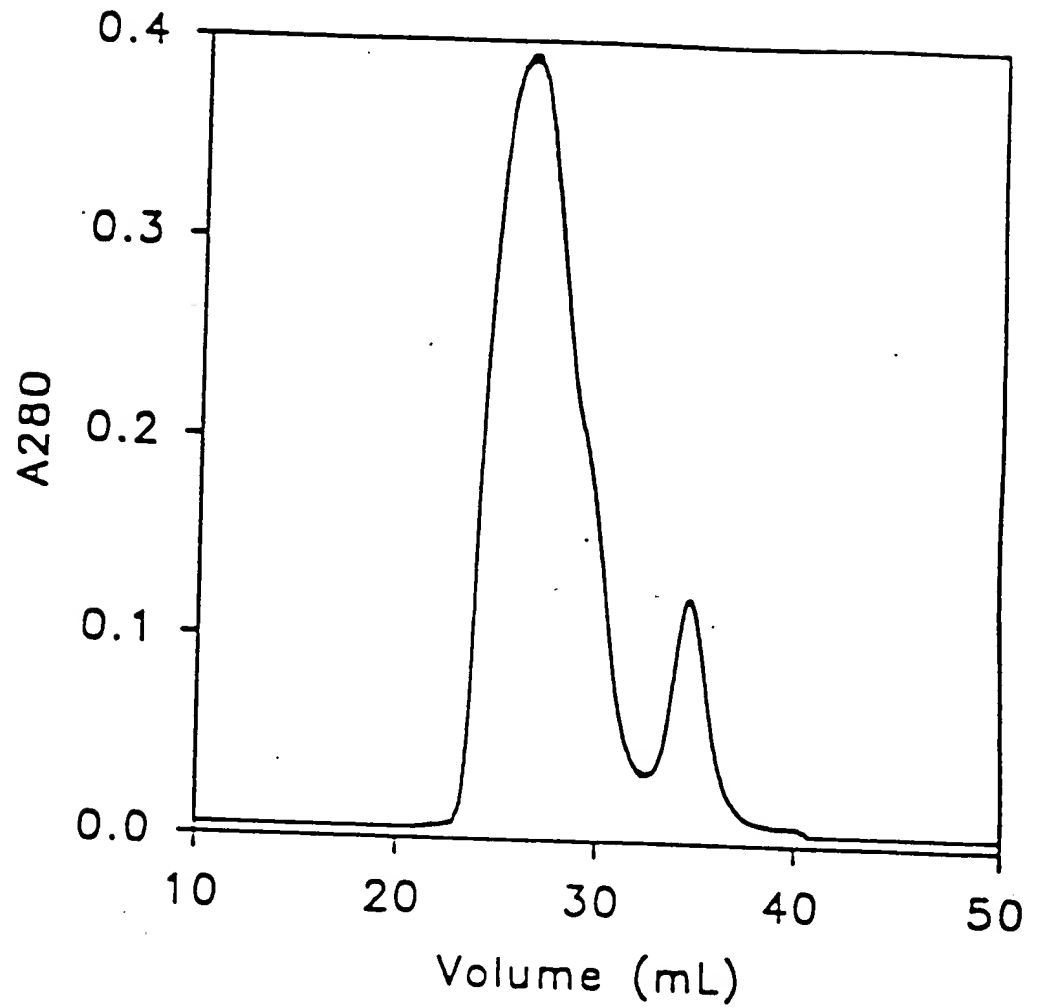


FIG. 40B

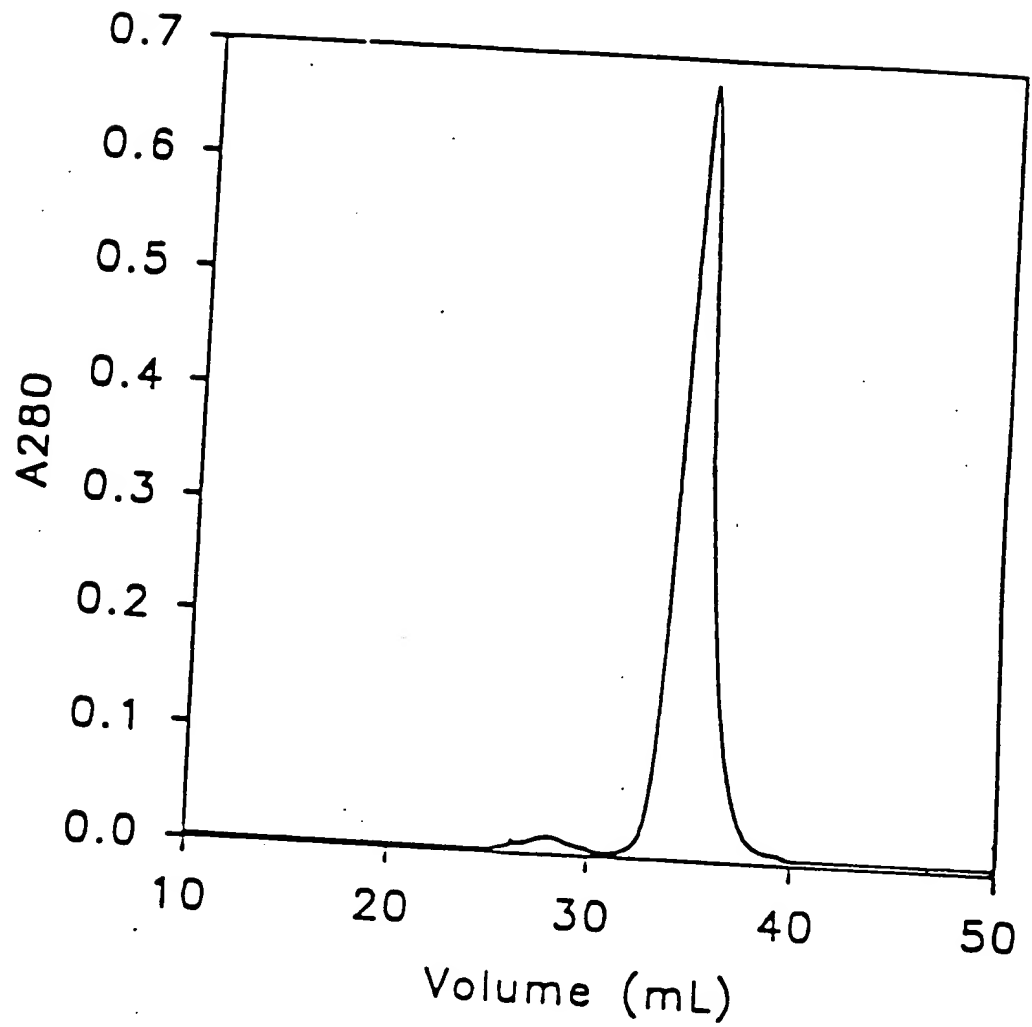


FIG. 41

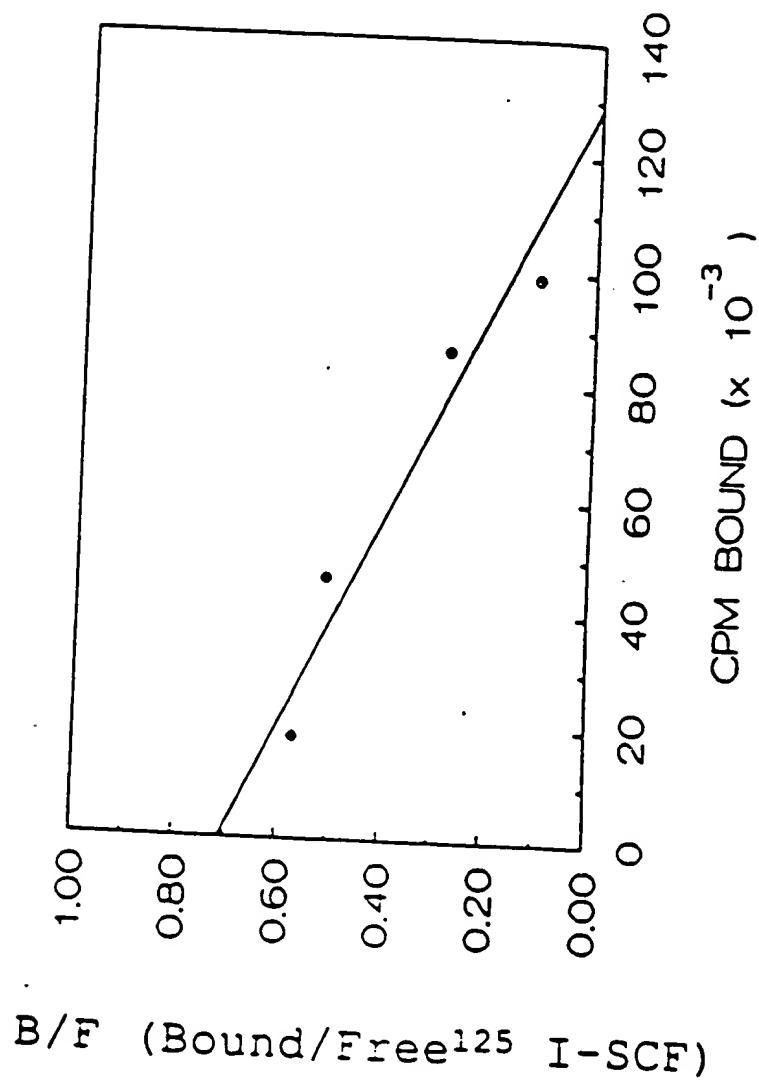


FIG. 42A

```
CCGCCTCGCCGCGAGACTAGAACGGCTGCGGGAAGCAGGACAGTGAGAGGGCGCTGCCG 61
TCGGGGCTACCCCAATGCGTGGACTATCTGCCGCCGCTGTTCGTGCAATATGCTGGAGCTCCA 122
GAACAGCTAAACGGAGTCGCCACACCACCTGTTCGTGCTGGATCGCAGCGCTGCCCTTTCCTT 183

-25      -20      1
Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln
ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG 228

-10      10      20
Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg
CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG 273

Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala 20
AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTG GCA 318

Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly
AAT CTT CCA AAA GAC GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG 363

Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val 50
ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA 408

Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn
CAA TTG TCA GAC AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT 453

60
```

FIG. 42B

Ile	Ser	Glu	Gly	Leu	Ser	Asn	Tyr	Ser	Ile	Ile	Asp	Lys	Leu	Val	80
ATT	TCT	GAA	GGC	TTG	AGT	AAT	TAT	TCC	ATC	ATA	GAC	AAA	CTT	GTG	498
Asn	Ile	Val	Asp	Asp	Leu	Val	Glu	Cys	Val	Lys	Glu	Asn	Ser	Ser	
AAT	ATA	GTG	GAT	GAC	CTT	GTG	GAG	TGC	GTG	AAA	GAA	AAC	TCA	TCT	543
Lys	Asp	Leu	Lys	Lys	Ser	Phe	Lys	Ser	Pro	Glu	Pro	Arg	Leu	Phe	110
AAG	GAT	CTA	AAA	AAA	TCA	TTC	AAG	AGC	CCA	GAA	CCC	AGG	CTC	TTT	588
Thr	Pro	Glu	Glu	Phe	Phe	Arg	Ile	Phe	Asn	Arg	Ser	Ile	Asp	Ala	
ACT	CCT	GAA	GAA	TTC	TTT	AGA	ATT	TTT	AAT	AGA	TCC	ATT	GAT	GCC	633
Phe	Lys	Asp	Phe	Val	Val	Ala	Ser	Glu	Thr	Ser	Asp	Cys	Val	Val	140
TTC	AAG	GAC	TTT	GTA	GTG	GCA	TCT	GAA	ACT	AGT	GAT	TGT	GTG	GTT	678
Ser	Ser	Thr	Leu	Ser	Pro	Glu	Lys	Asp	Ser	Arg	Val	Ser	Val	Thr	
TCT	TCA	ACA	TTA	AGT	CCT	GAG	AAA	GAT	TCC	AGA	GTC	AGT	GTC	ACA	723

FIG. 42C

Lys	Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala	Ser	Ser	Leu	Arg	Asn	170
AAA	CCA	TTT	ATG	TTA	CCC	CCT	GT	GCA	GCC	AGC	TCC	CTT	AGG	AAT	768
Asp	Ser	Ser	Ser	Asn	Arg	Lys	Ala	Lys	Asn	Pro	Pro	Gly	Asp		
GAC	AGC	AGT	AGC	AAT	AGG	AAG	GCC	AAA	AAT	CCC	CCT	GGA	GAC	813	
Ser	Ser	Leu	His	Trp	Ala	Ala	Met	Ala	Leu	Pro	Ala	Leu	Phe	Ser	
TCC	AGC	CTA	CAC	TGG	GCA	GCC	ATG	GCA	TTG	CCA	GCA	TTG	TTT	TCT	858
Leu	Ile	Ile	Gly	Phe	Ala	Phe	Gly	Ala	Leu	Tyr	Trp	Lys	Lys	Arg	
CTT	ATA	ATT	GGC	TTT	GCT	TTT	GGA	GCC	TTA	TAC	TGG	AAG	AAG	AGA	903
Gln	Pro	Ser	Leu	Thr	Arg	Ala	Val	Glu	Asn	Ile	Gln	Ile	Asn	Glu	
CAG	CCA	AGT	CTT	ACA	AGG	GCA	GTT	GAA	AAT	ATA	CAA	ATT	AAT	GAA	948
Glu	Asp	Asn	Glu	Ile	Ser	Met	Leu	Gln	Glu	Lys	Glu	Arg	Glu	Phe	
GAG	GAT	AAT	GAG	ATA	AGT	ATG	TTG	CAA	GAG	AAA	GAG	AGA	GAG	TTT	993
Gln	Glu	Val	End												
CAA	GAA	GTG	TAA												
														TTGTGGCTTGTATCAACACTGTTACTTTTCGTACATTGGC	1044

FIG. 42D

TGGTAACAGTTTCATGTTTGCTTCATAAATGAAGCAGCCTTTAAACAATTCATATTCTGTC 1104
TGGAGTGACAGACCAACATCTTTATCTGTTCTTGCTACCCATGACTTTATATGGATGATTC 1164
AGAAATTGGAAACAGAAATGTTTACTGTGAAACTGGCAGCTGAATTAATCATCTATAAAGAA 1224
GAACTTGCAATGGAGCAGGACTCTATTTTAAGGACTGCGGGGACTTGGGTCTCATTTAGAAC 1284
TTGCAGCTGATGTTGGAAGAGAAAGCACCGTGTCTCAGACTGCATGTACCATTTGCATGGC 1344
TCCAGAAATGCTCTAAATGCTGAAAAAACACCTAGCTTTATTCTTCAGATACAAACTGCCAG 1404

FIG. 43

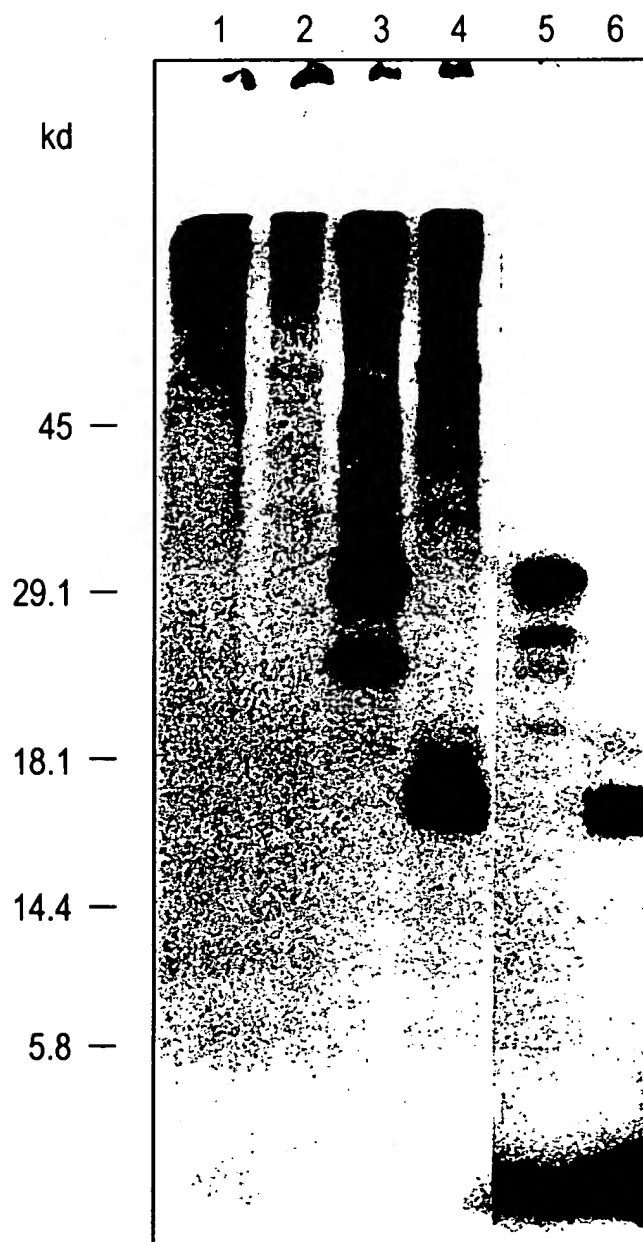


FIG. 44A

```

AGCAGGGACAGTGGAGAGGGCGCTGCGCTC 30
GGGCTACCCAAATGCGTGGACTATCTGCCCGCGCTGTTTCGTGCAATATGCTGGAGCTCCAG 90
AACAGCTAAACGGAGTCGCCACACCACTGTTGTGCTGGATCGCAGCGCTGCCTTTCCCTT 150
-25
Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln
ATG AAG AAG ACA ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG 195
-10
Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg
CTG CTC CTA TTT AAT CCT CTC CTC GTC AAA ACT GAA GGG ATC TGC AGG 240
10
Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala
AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTG GCA 285
30
Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly
AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG 330
40
Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val
ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA 375
50
```

Gln	Leu	Ser	Asp	Ser	Leu	Thr	Asp	Leu	Leu	Asp	Lys	Phe	Ser	Asn	420
CAA	TTG	TCA	GAC	AGC	TTG	ACT	GAT	CTT	CTG	GAC	AAG	TTT	TCA	AAT	
60															
Ile	Ser	Glu	Gly	Leu	Ser	Asn	Tyr	Ser	Ile	Ile	Asp	Lys	Leu	Val	80
ATT	TCT	GAA	GGC	TTG	AGT	AAT	TAT	TCC	ATC	ATA	GAC	AAA	CTT	GTG	
70															
Asn	Ile	Val	Asp	Asp	Leu	Val	Glu	Cys	Val	Lys	Glu	Asn	Ser	Ser	465
AAAT	ATA	GTG	GAT	GAC	CTT	GTG	GAG	TGC	GTG	AAA	GAA	AAC	TCA	TCT	
90															
Lys	Asp	Leu	Lys	Lys	Ser	Phe	Lys	Ser	Pro	Glu	Pro	Arg	Leu	Phe	110
AAAG	GAT	CTA	AAA	AAA	TCA	TTC	AAG	AGC	CCA	GAA	CCC	AGG	CTC	TTT	555
100															
Thr	Pro	Glu	Glu	Phe	Phe	Arg	Ile	Phe	Asn	Arg	Ser	Ile	Asp	Ala	600
ACT	CCT	GAA	GAA	TTC	TTT	AGA	ATT	TTT	AAT	AGA	TCC	ATT	GAT	GCC	
120															
Phe	Lys	Asp	Phe	Val	Val	Ala	Ser	Glu	Thr	Ser	Asp	Cys	Val	Val	140
TTC	AAG	GAC	TTT	GTA	GTG	GCA	TCT	GAA	ACT	AGT	GAT	TGT	GTG	GTT	645
130															
Ser	Ser	Thr	Leu	Ser	Pro	Glu	Lys	Gly	Lys	Ala	Lys	Asn	Pro	Pro	690
TCT	TCA	ACA	TTA	AGT	CCT	GAG	AAA	GGG	AAG	GCC	AAA	AAT	CCC	CCT	
150															

FIG. 44C

Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu	170
GGA GAC TCC AGC CTA CAC CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG	735
Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys	180
TTT TCT CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG	780
Lys Arg Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile	200
AAG AGA CAG CCA AGT CTT ACA AGG GCA GTT GAA AAT ATA CAA ATT	825
Asn Glu Glu Asp Asn Glu Ile Ser Met Leu Glu Glu Lys Glu Arg	210
AAT GAA GAG GAT AAT GAG ATA AGT ATG TTG CAA GAG AAA GAG AGA	870
Glu Phe Gln Glu Val End	220
GAG TTT CAA GAA GTG TAA TTGTGGCTTGTATCAACACTGTTACTTTCGTA	920
CATTGGCTGGTAACAGTTTCATGTTTGCTTCATAAATGAAGCAGCTTTAAACAATTCATA	980
TTCTGTCTGGAGTGACAGACCACATCTTTATCTGTCTTGCTACCCATGACTTTATATGG	1040
ATGATTCAAGAAATTGGAACAGAAATGTTTTACTGTGAAACTGGCACTGA	1088

FIG. 45

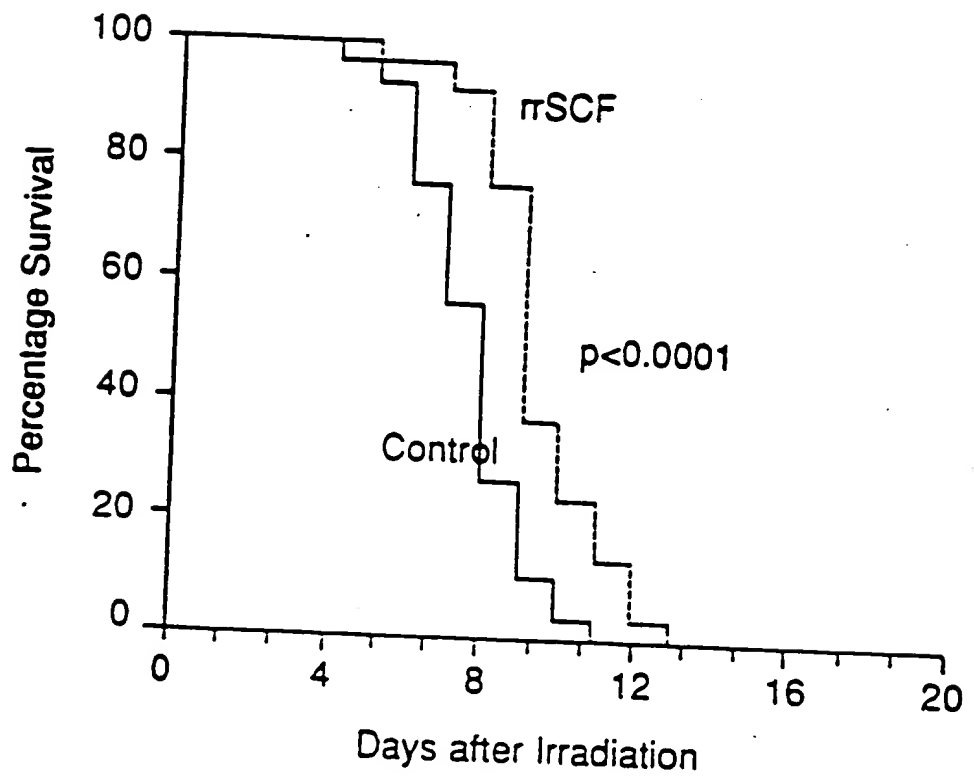
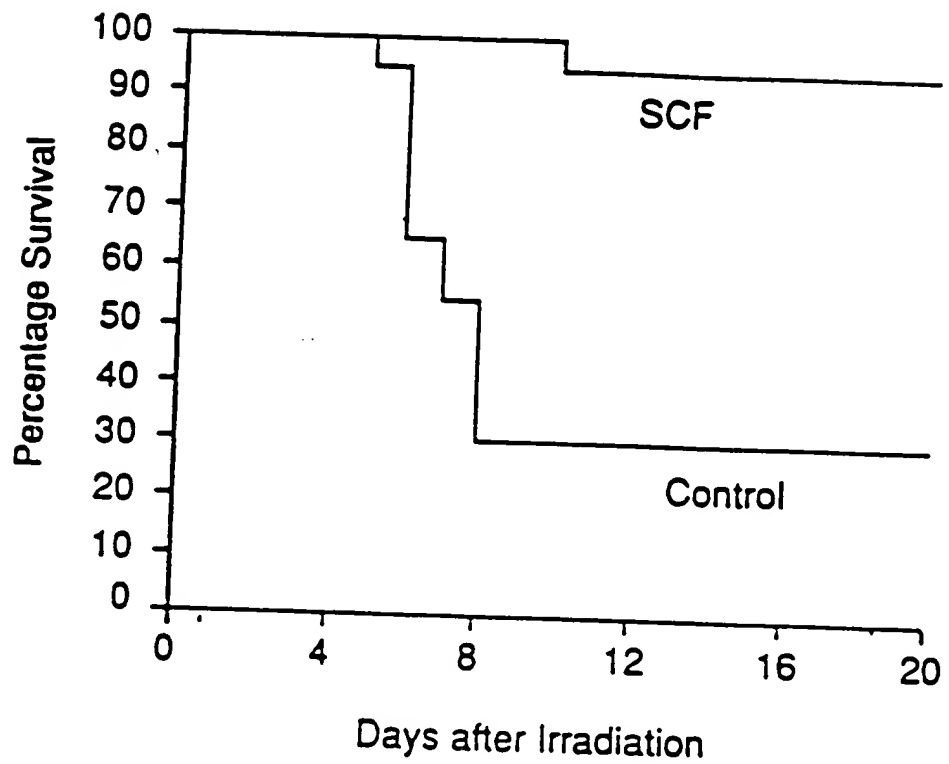
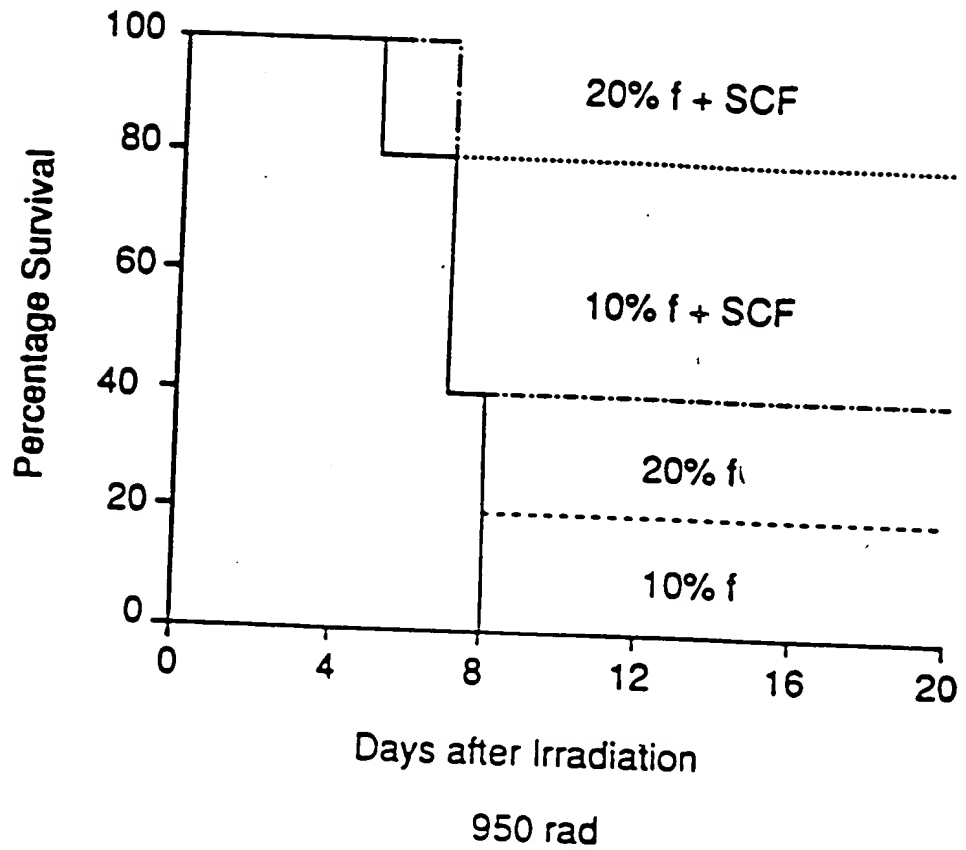


FIG. 46



850 RADS; 5% of femur transplanted

FIG. 47



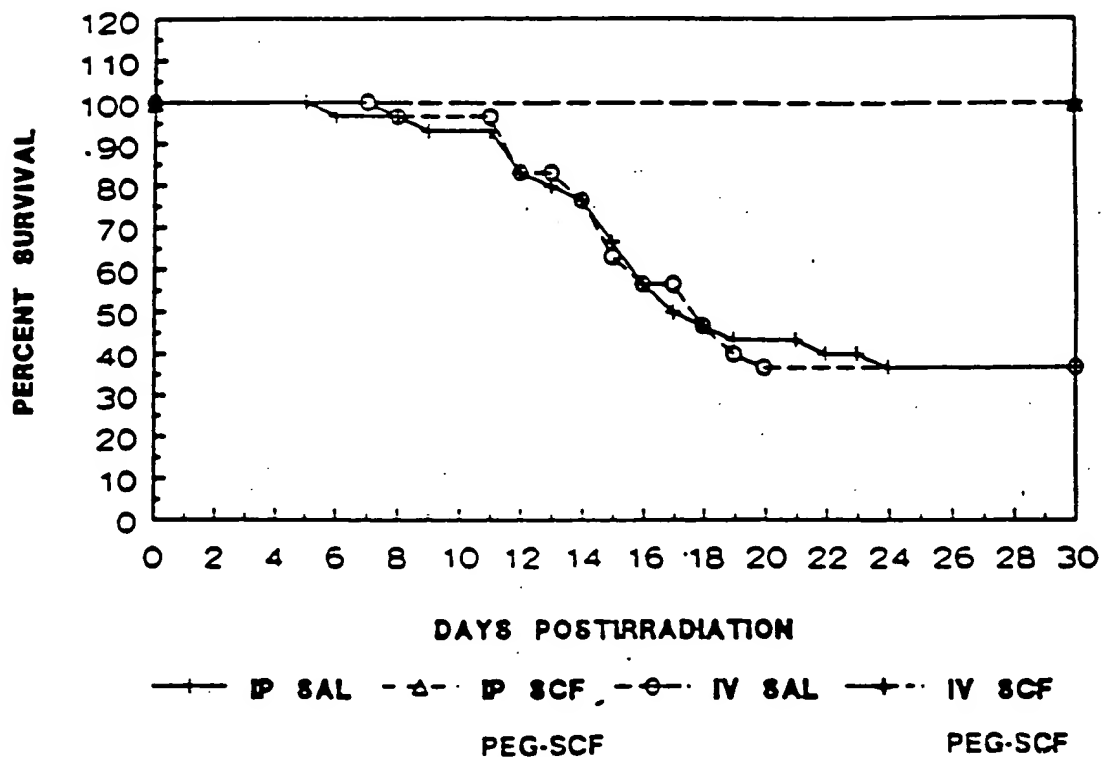


FIG. 49

SCF RADIOPROTECTION (1159 RAD)
Normal Female BDF1 mice

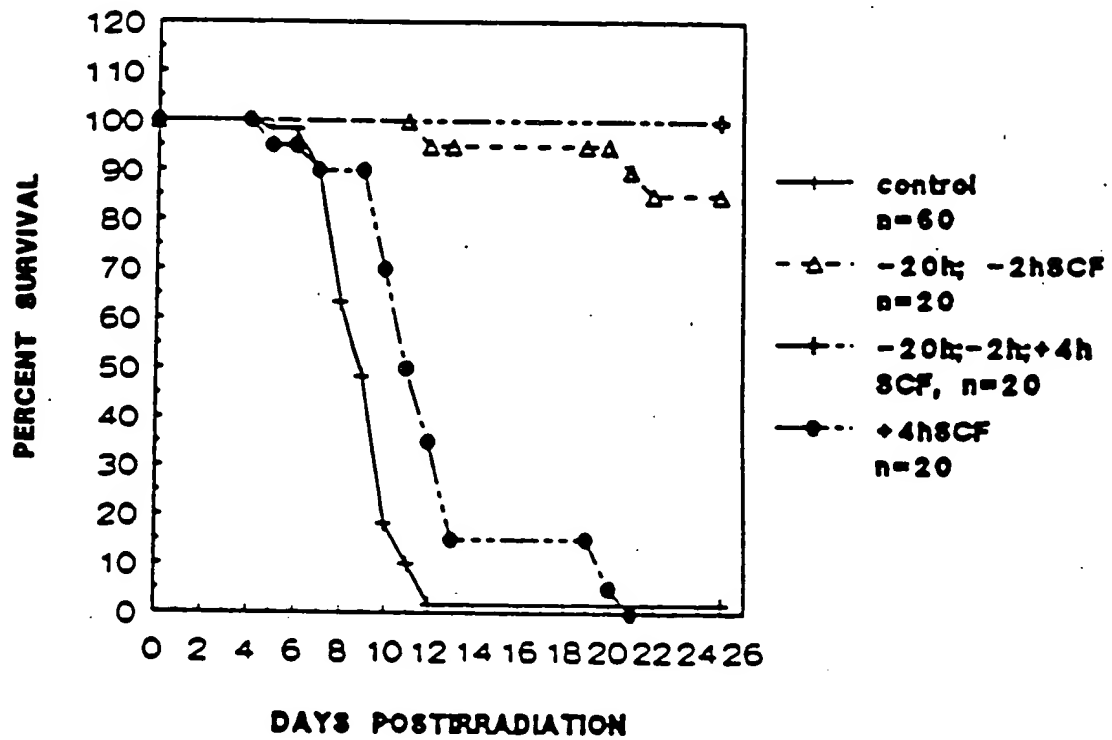


FIG. 50

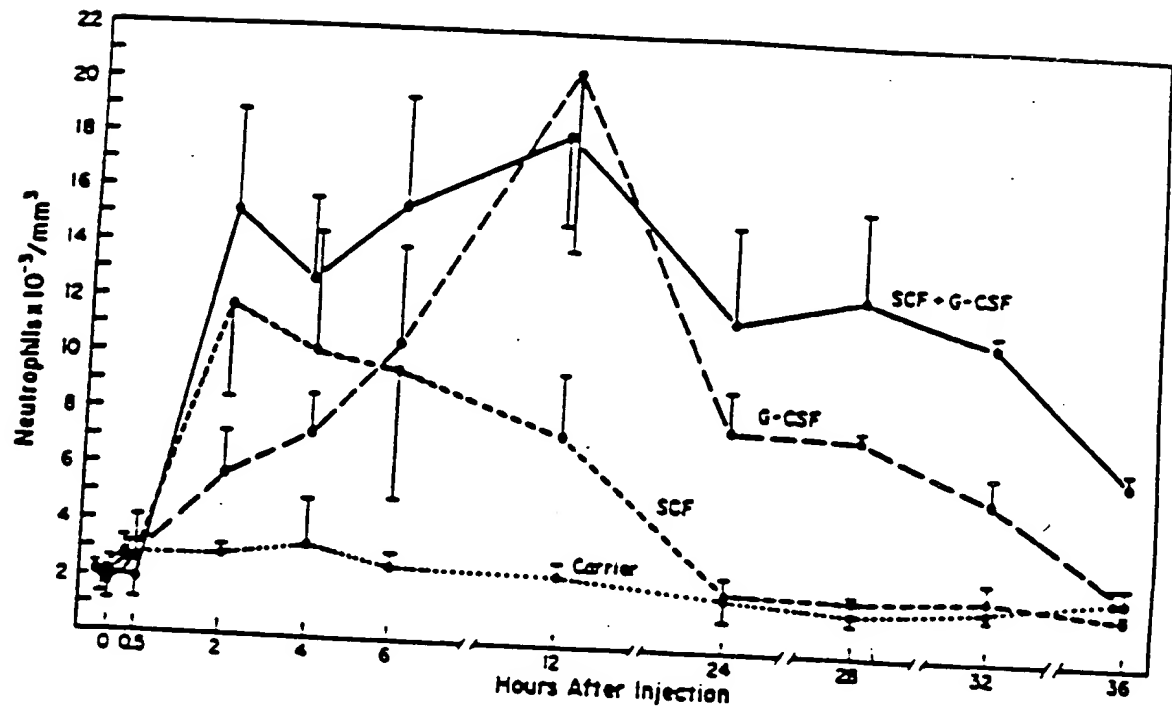


FIG. 51

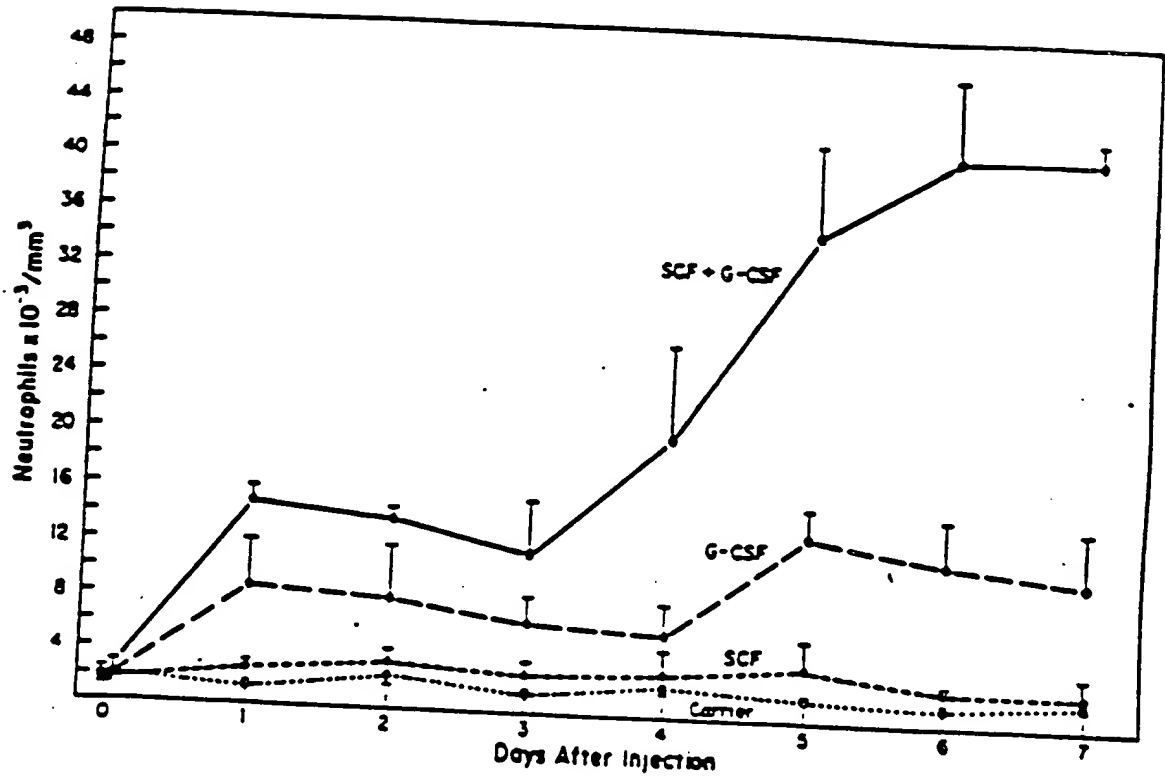


FIG. 52

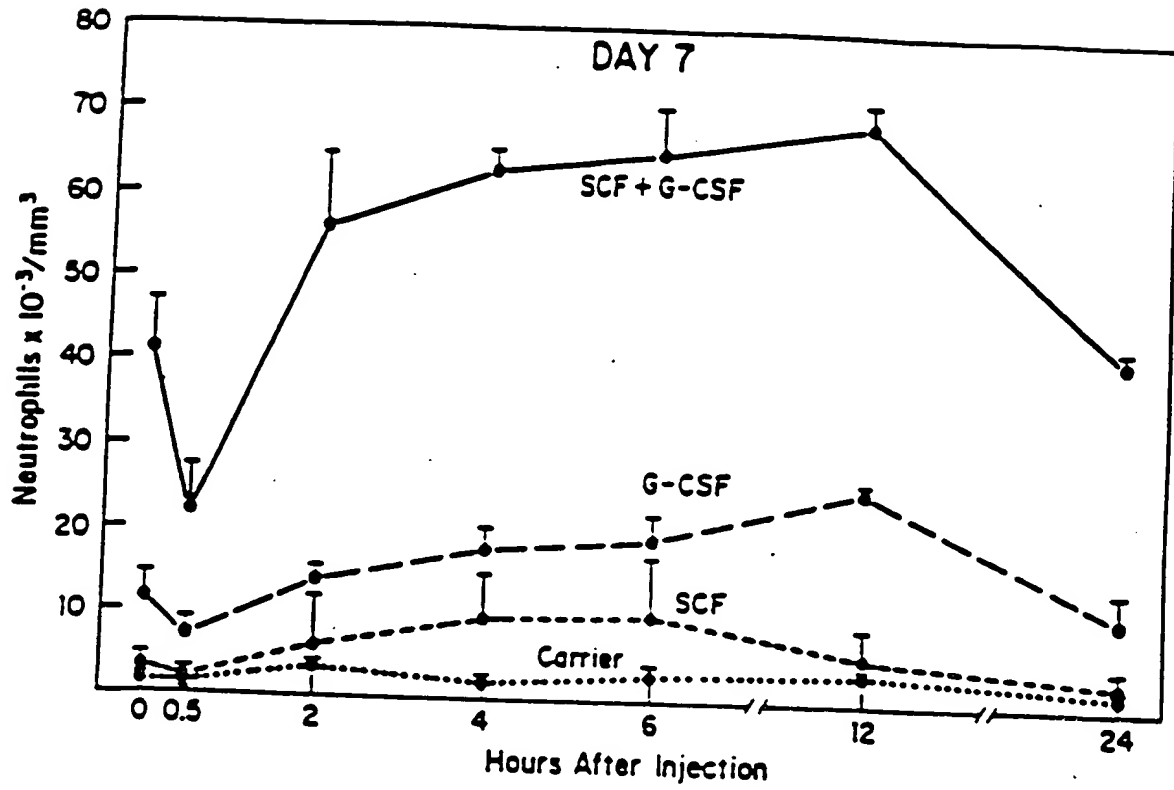


FIG. 53

in vivo Administration of SCF-Platelet Counts

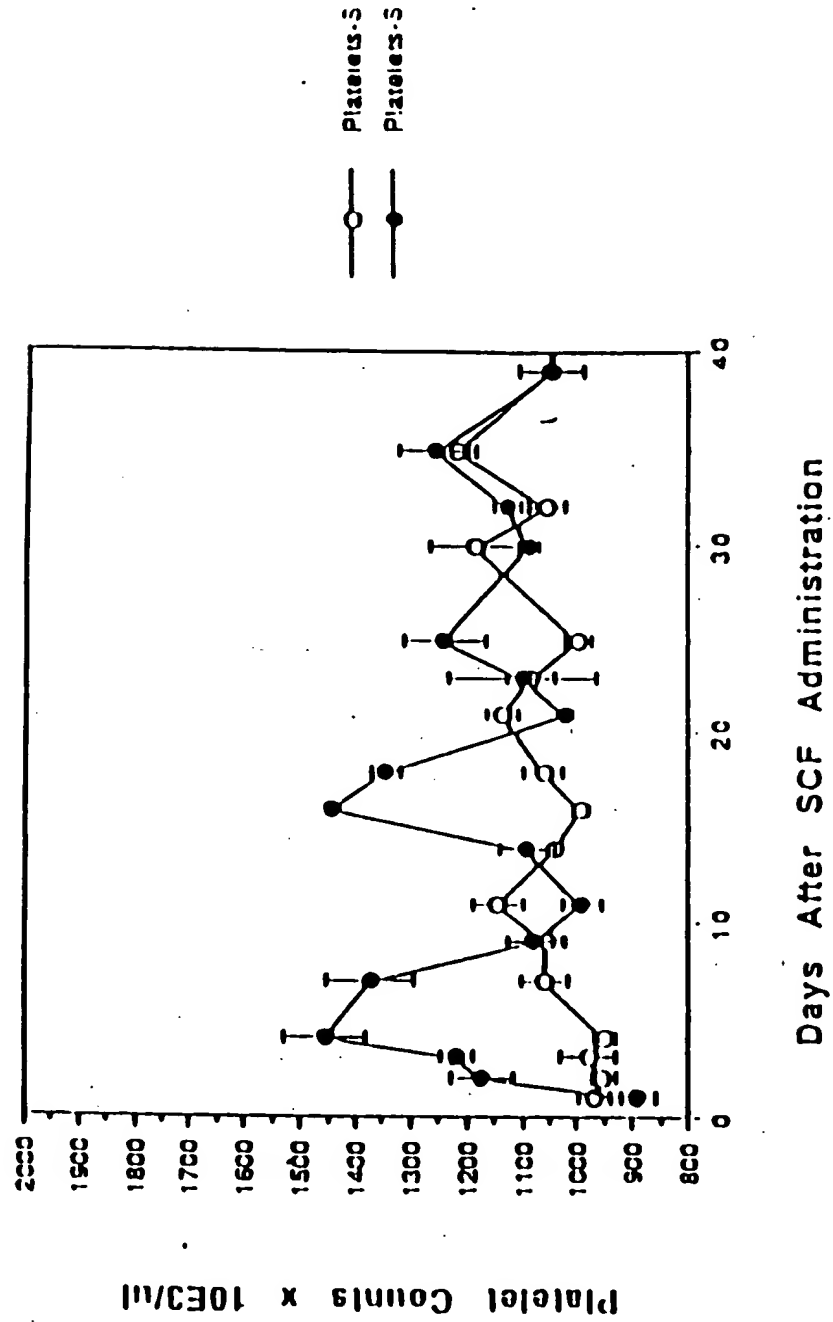


FIG. 54

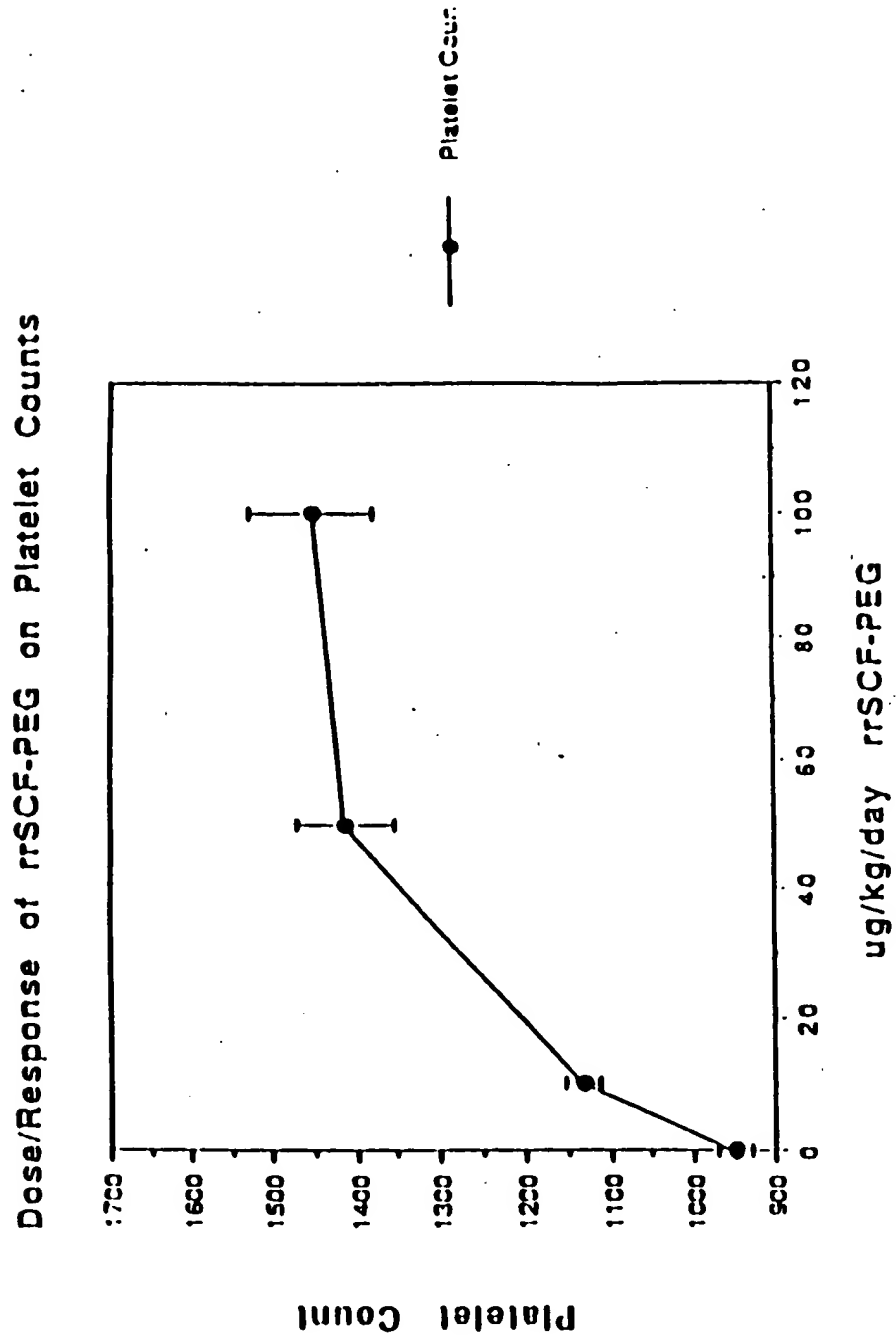


FIG. 55

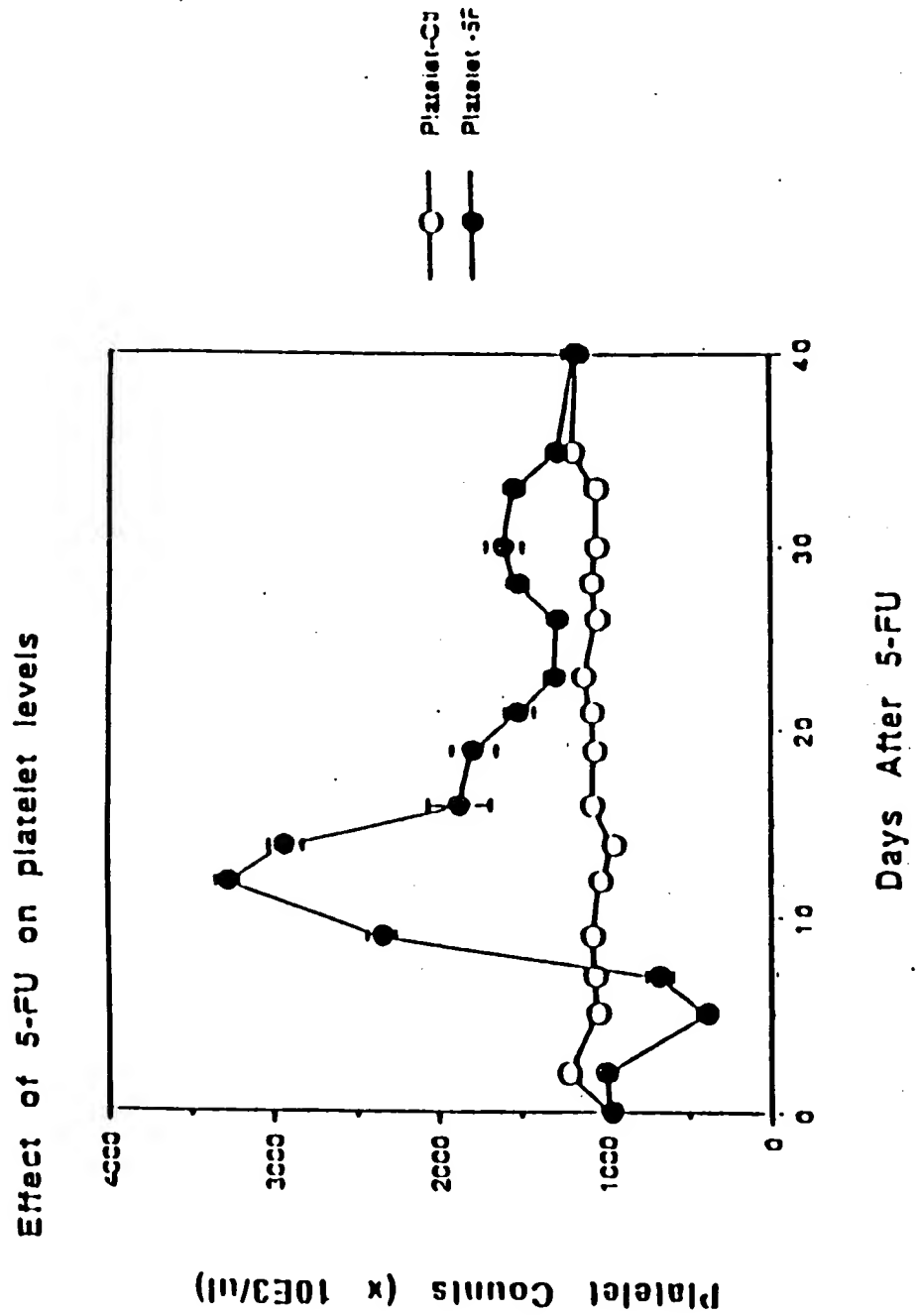
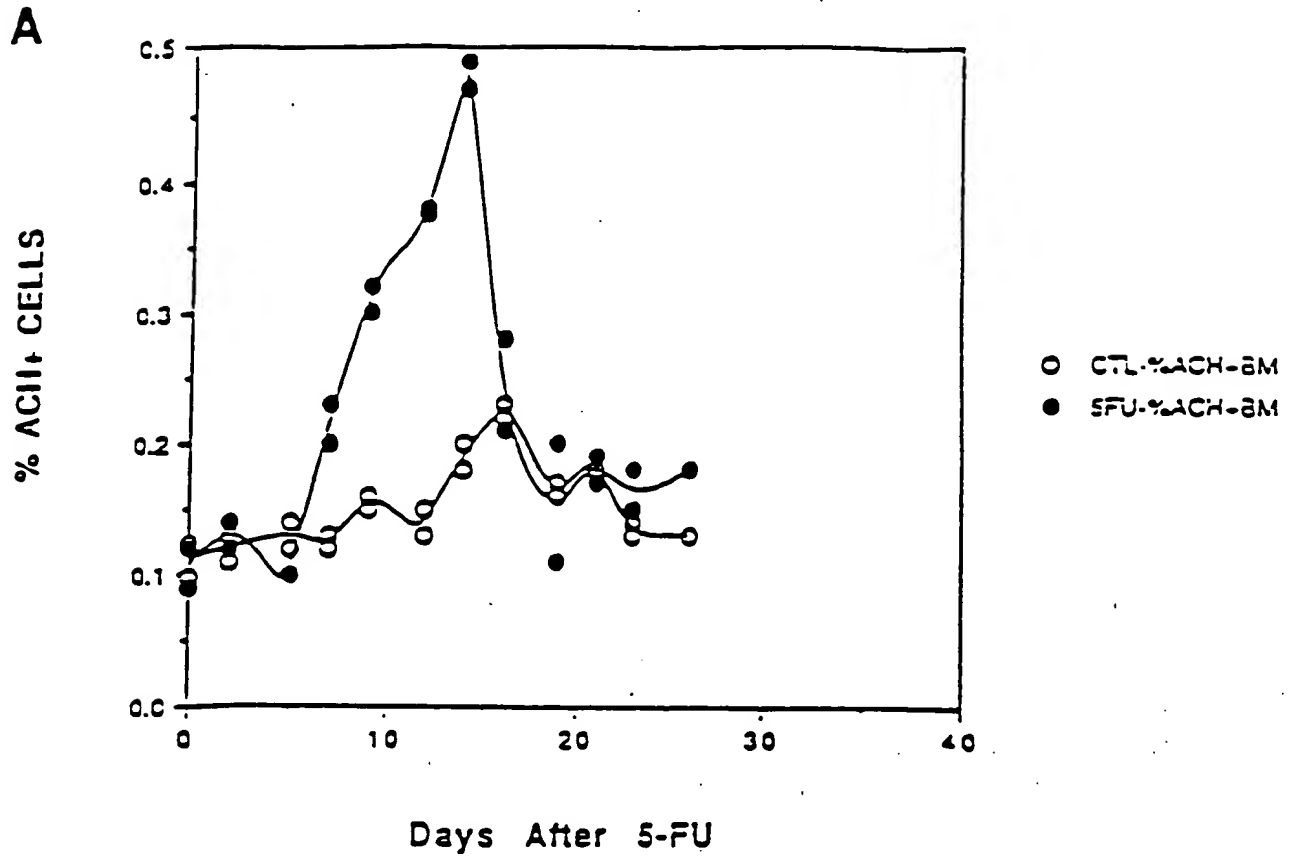


FIG. 56

5-FU Effect on ACH+ Cells in Marrow



5-FU Effect on ACH+ Cells in Spleen

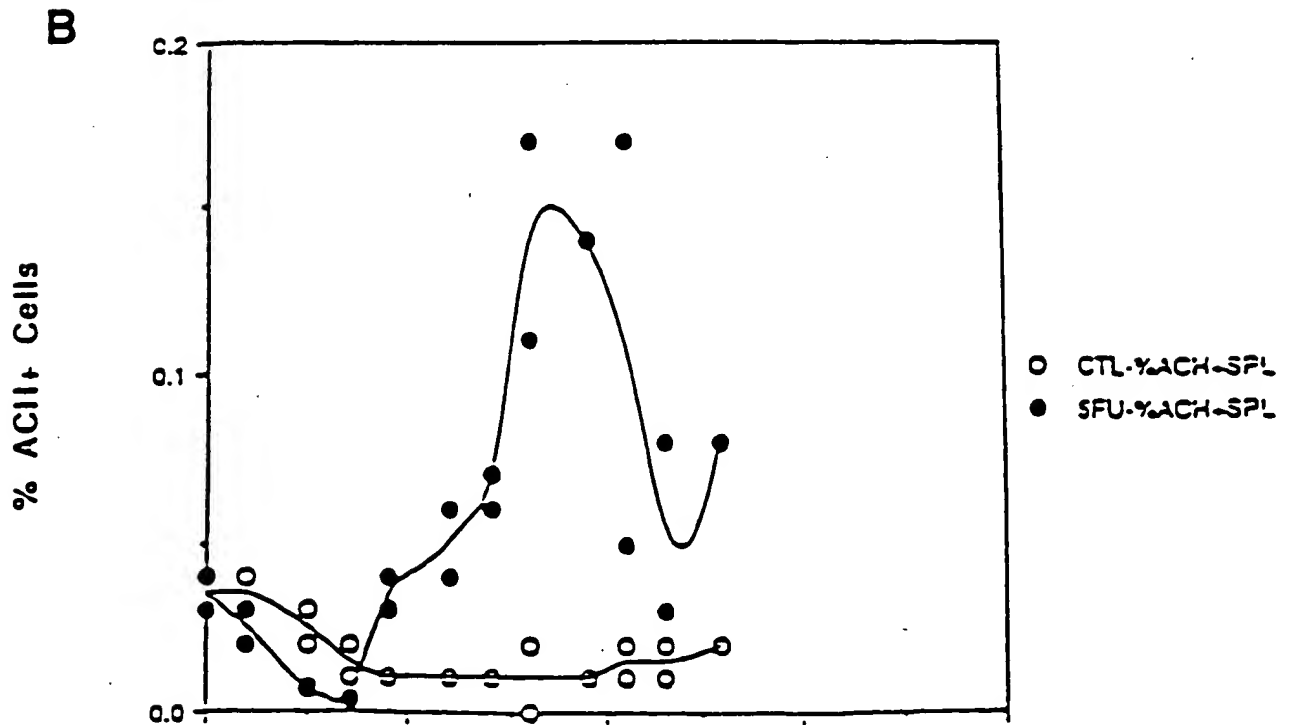


FIG. 57

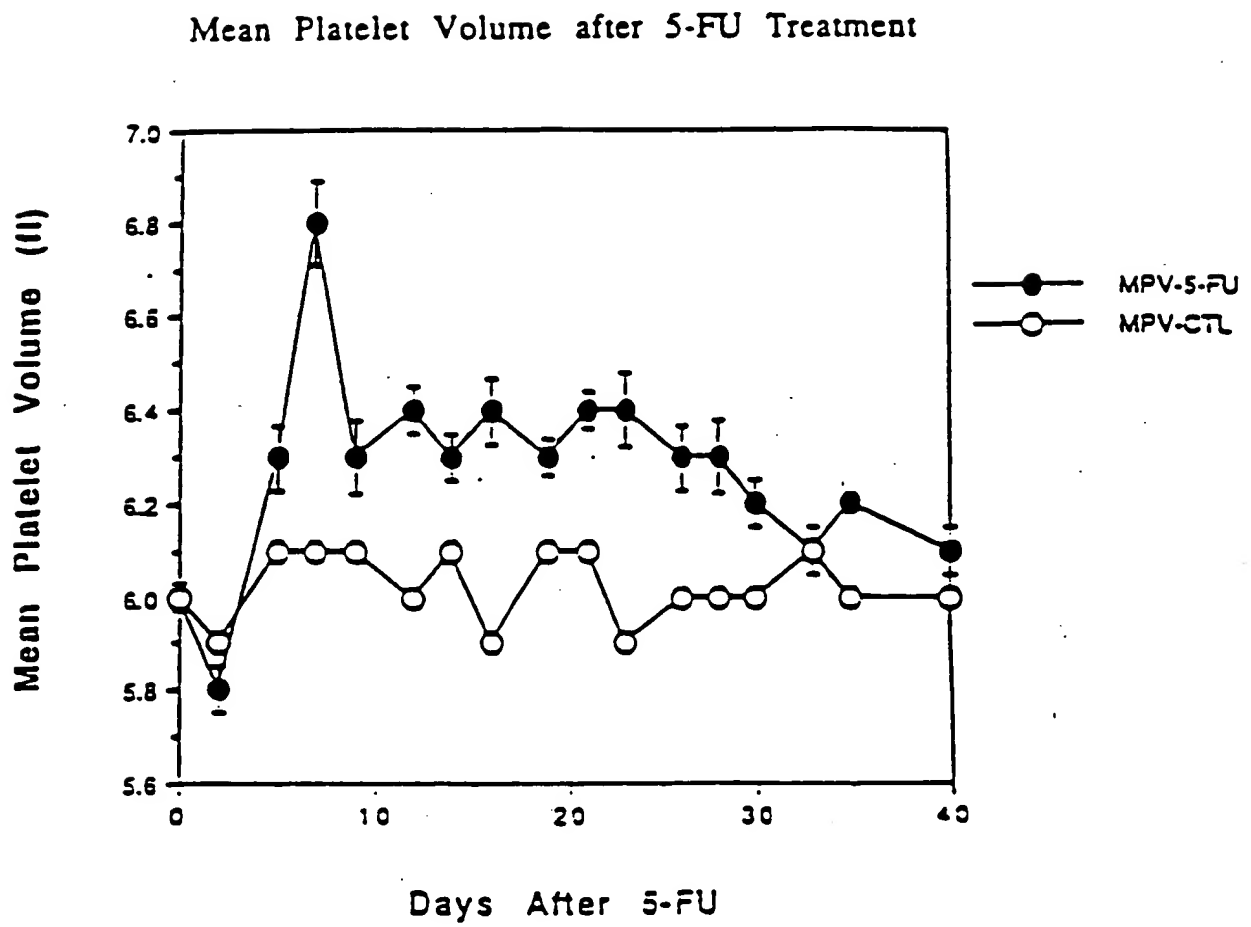


FIG. 58

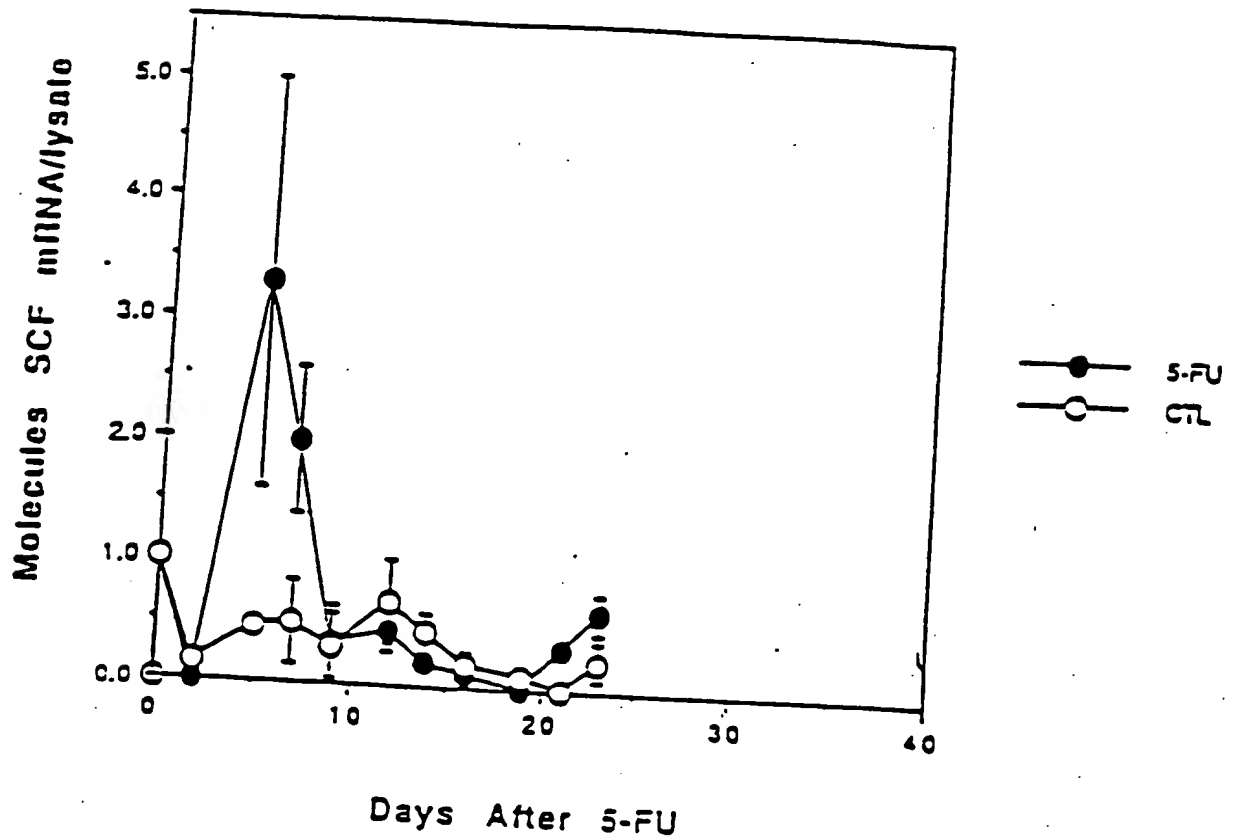


FIG. 59

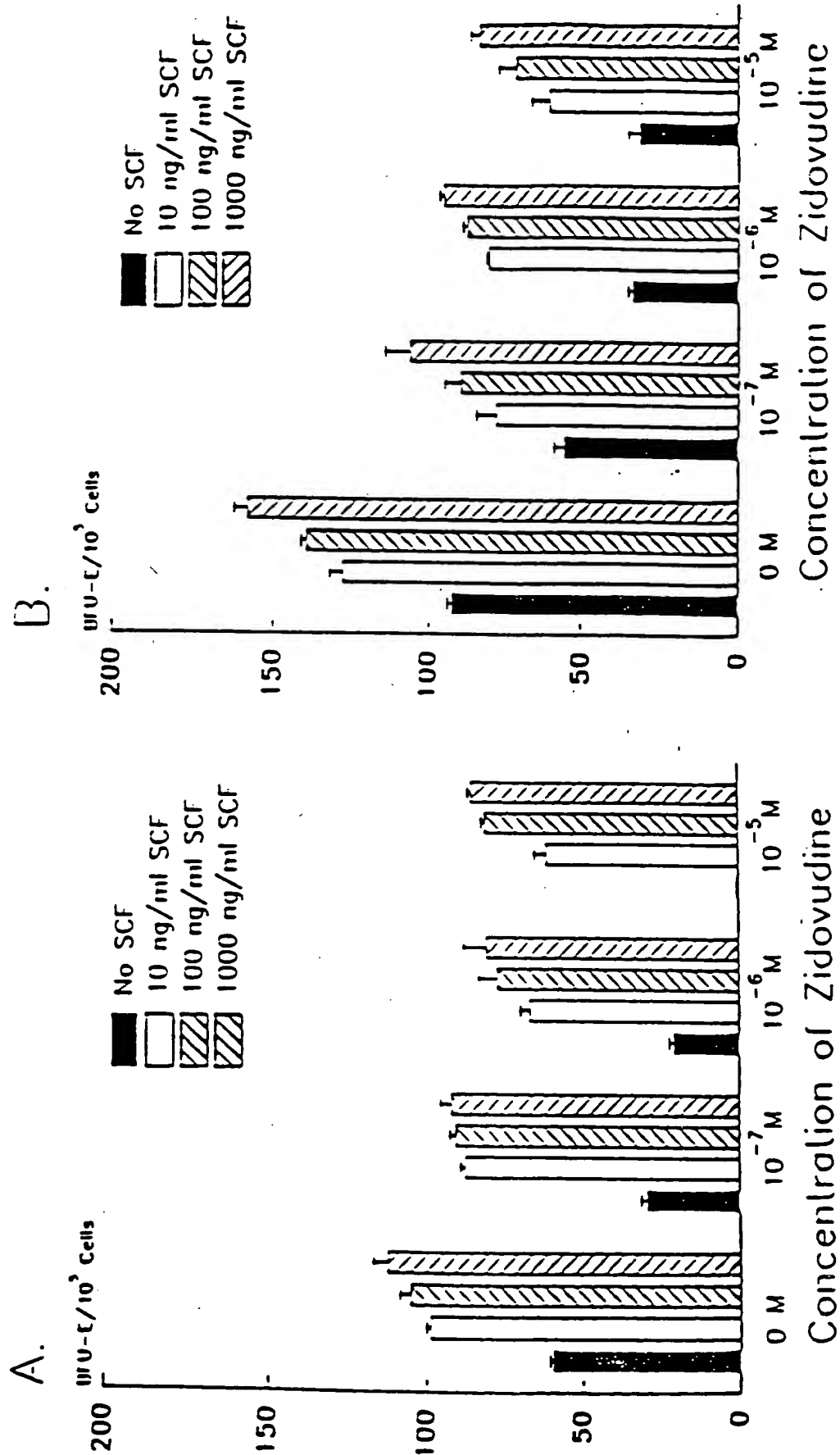


FIG. 60

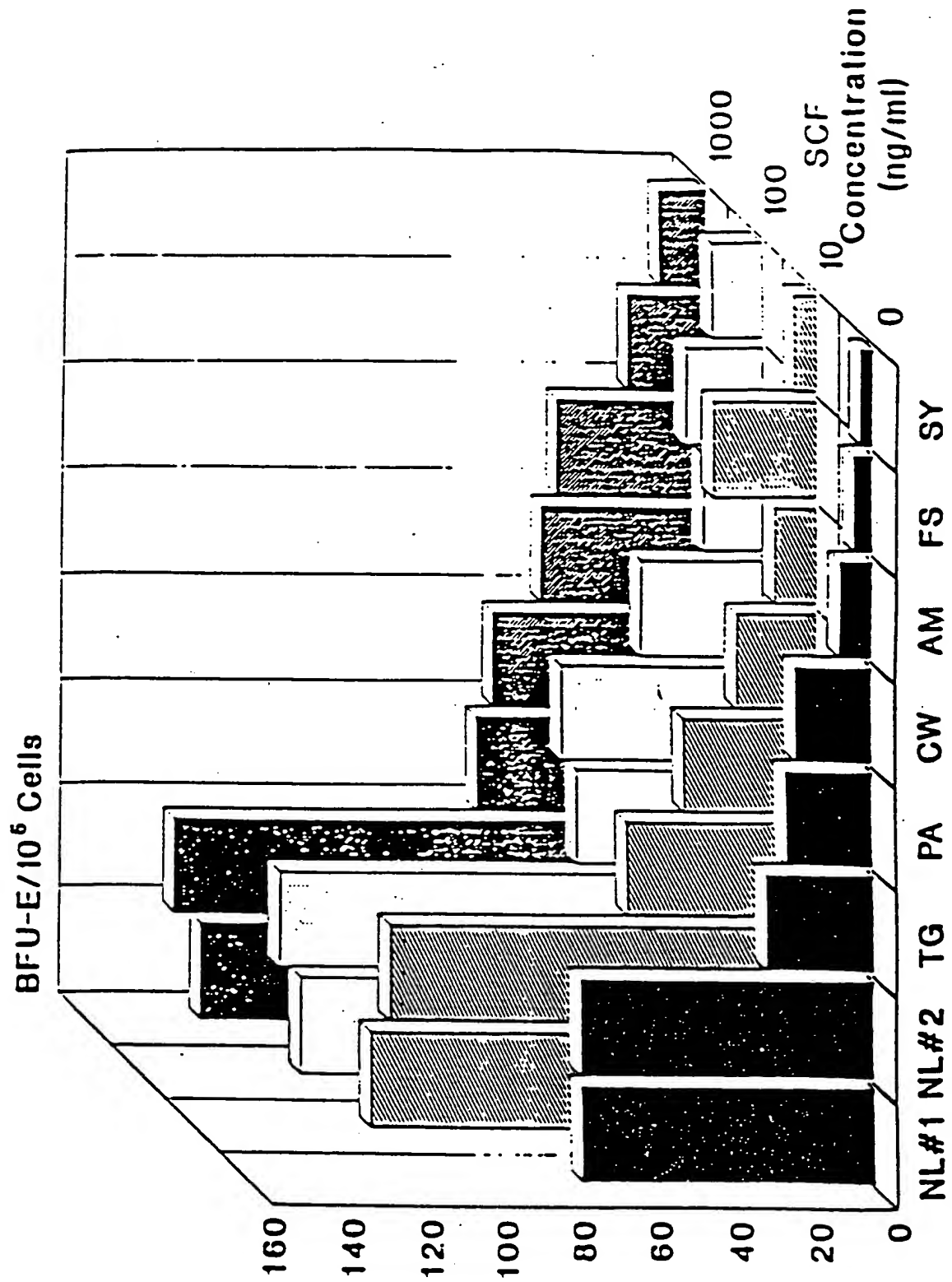


FIG. 61

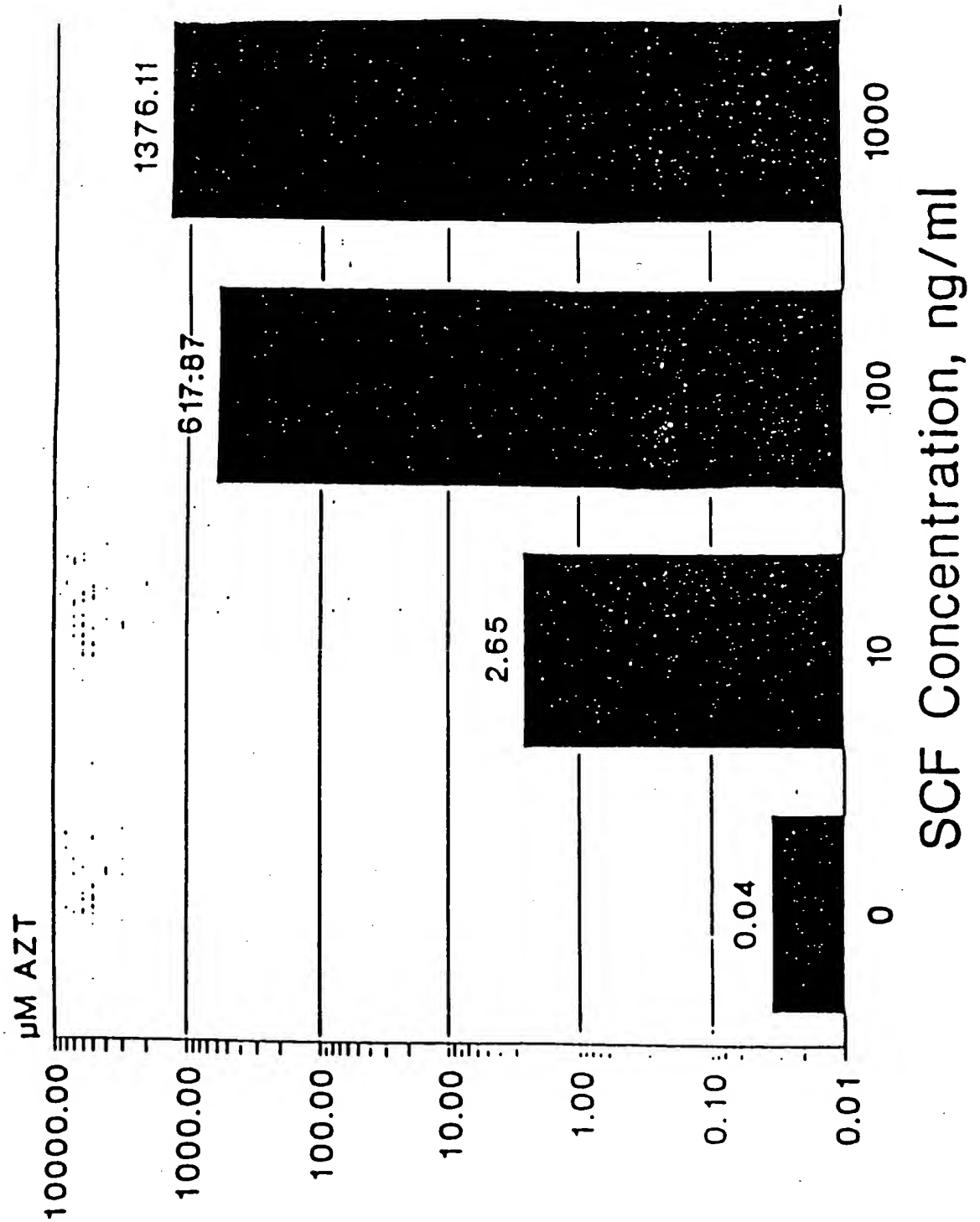


FIG. 62

EFFECT OF SCF ON AZT SUPPRESSION OF BMC

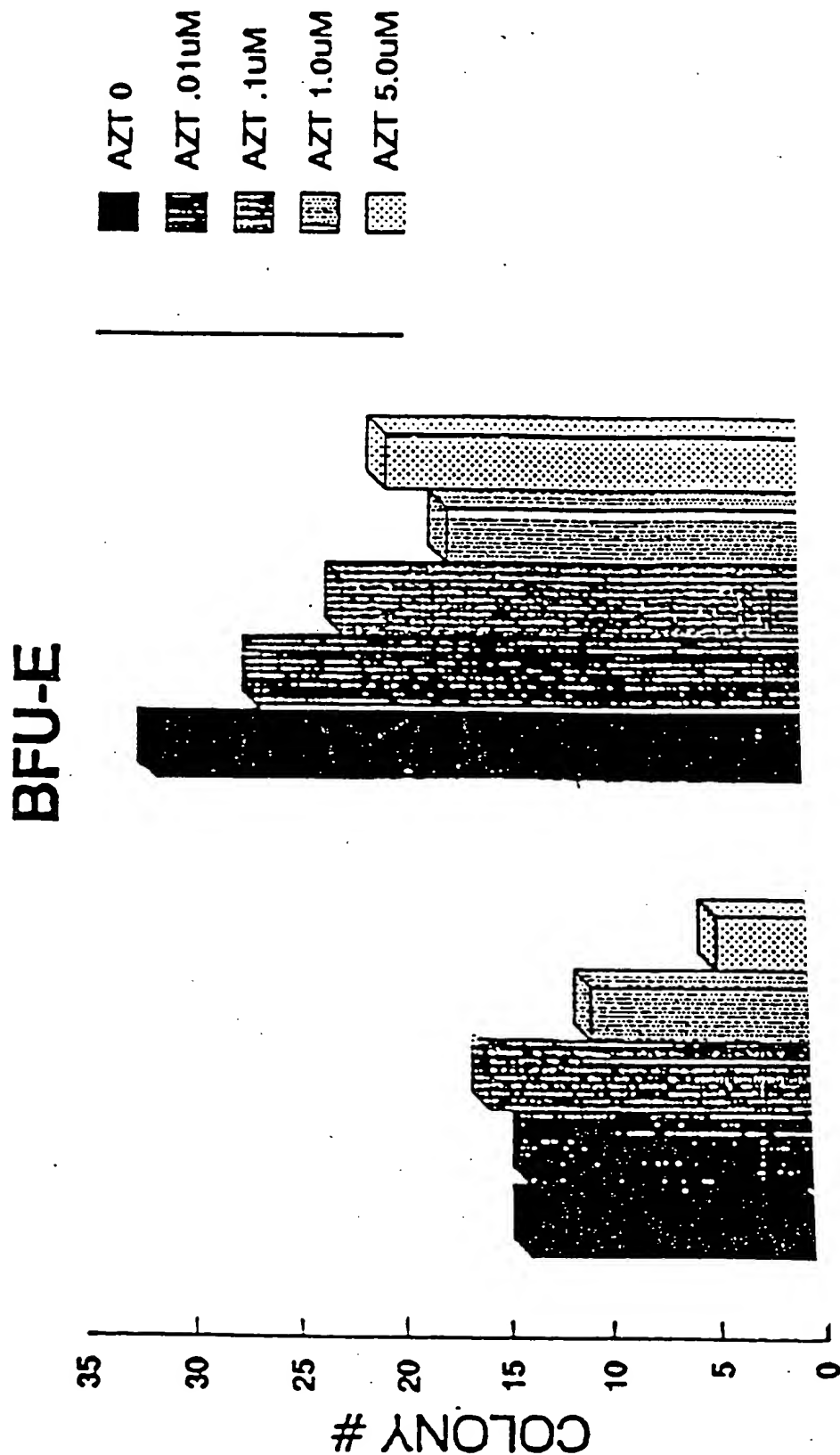


FIG. 63

EFFECT OF SCF ON AZT SUPPRESSION OF BMC

CFU-GM

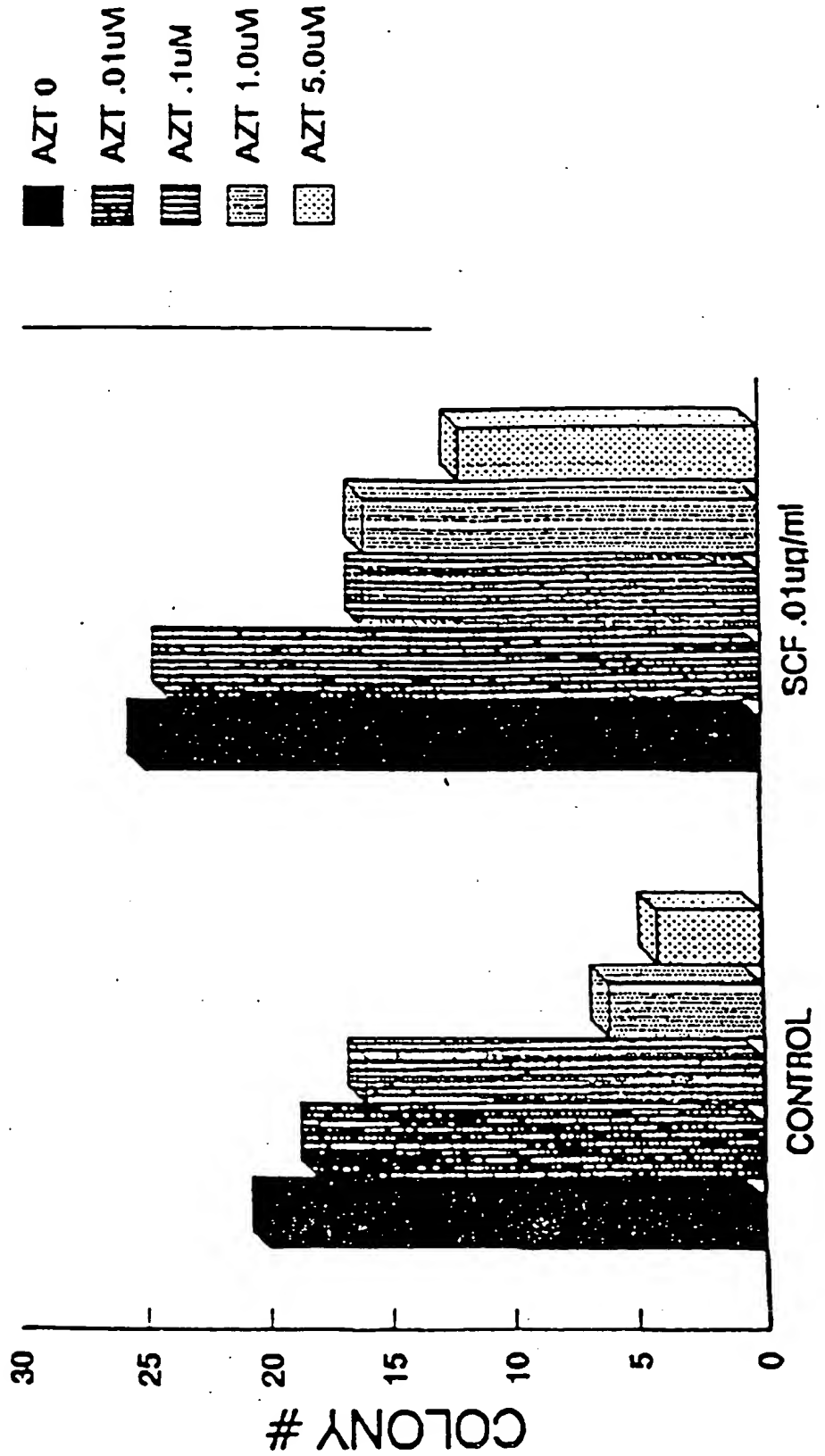


FIG. 64
EFFECT OF SCF ON GANCICLOVIR SUPPRESSION OF BMC

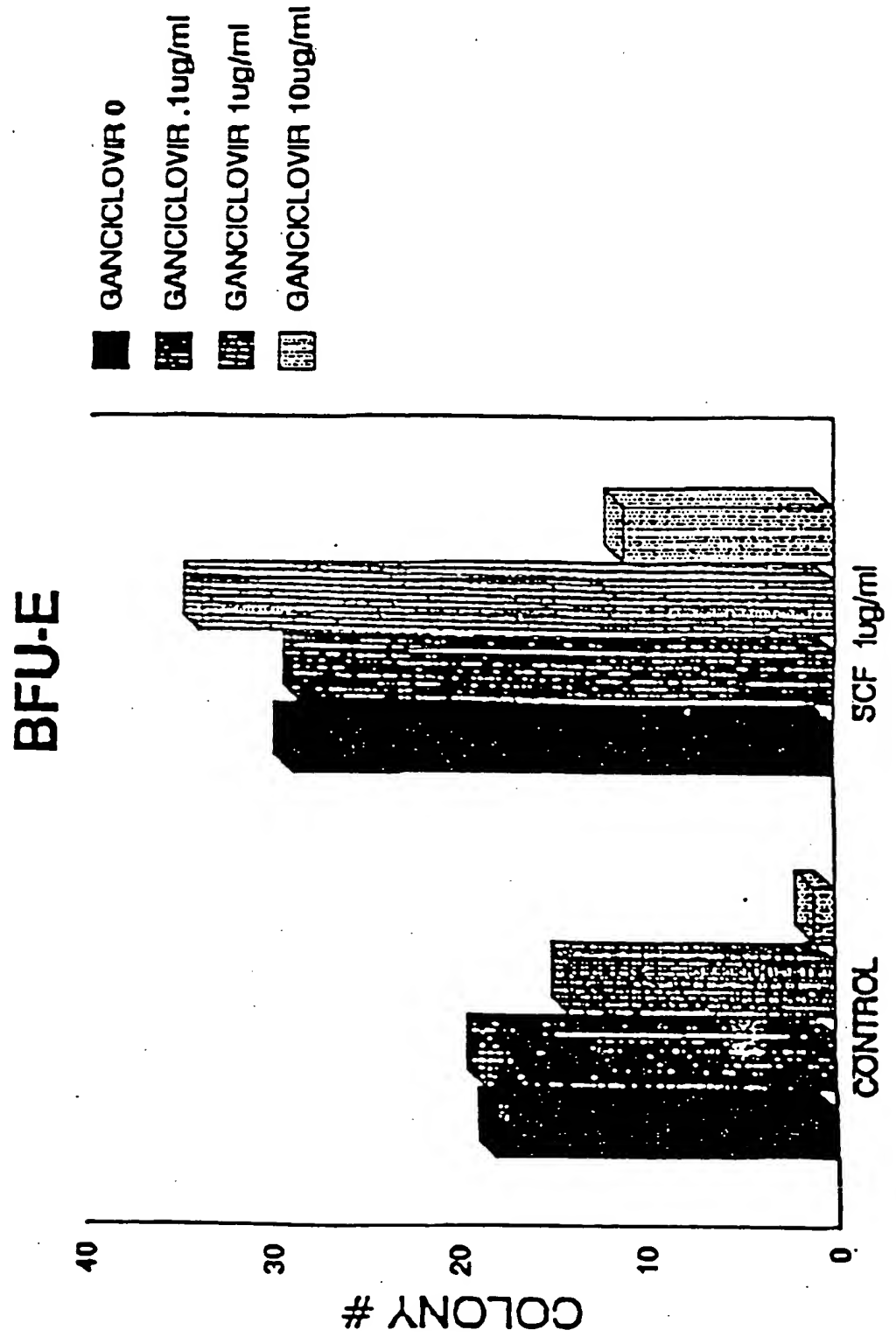


FIG. 65

EFFECT OF SCF ON GANCICLOVIR SUPPRESSION OF BMC

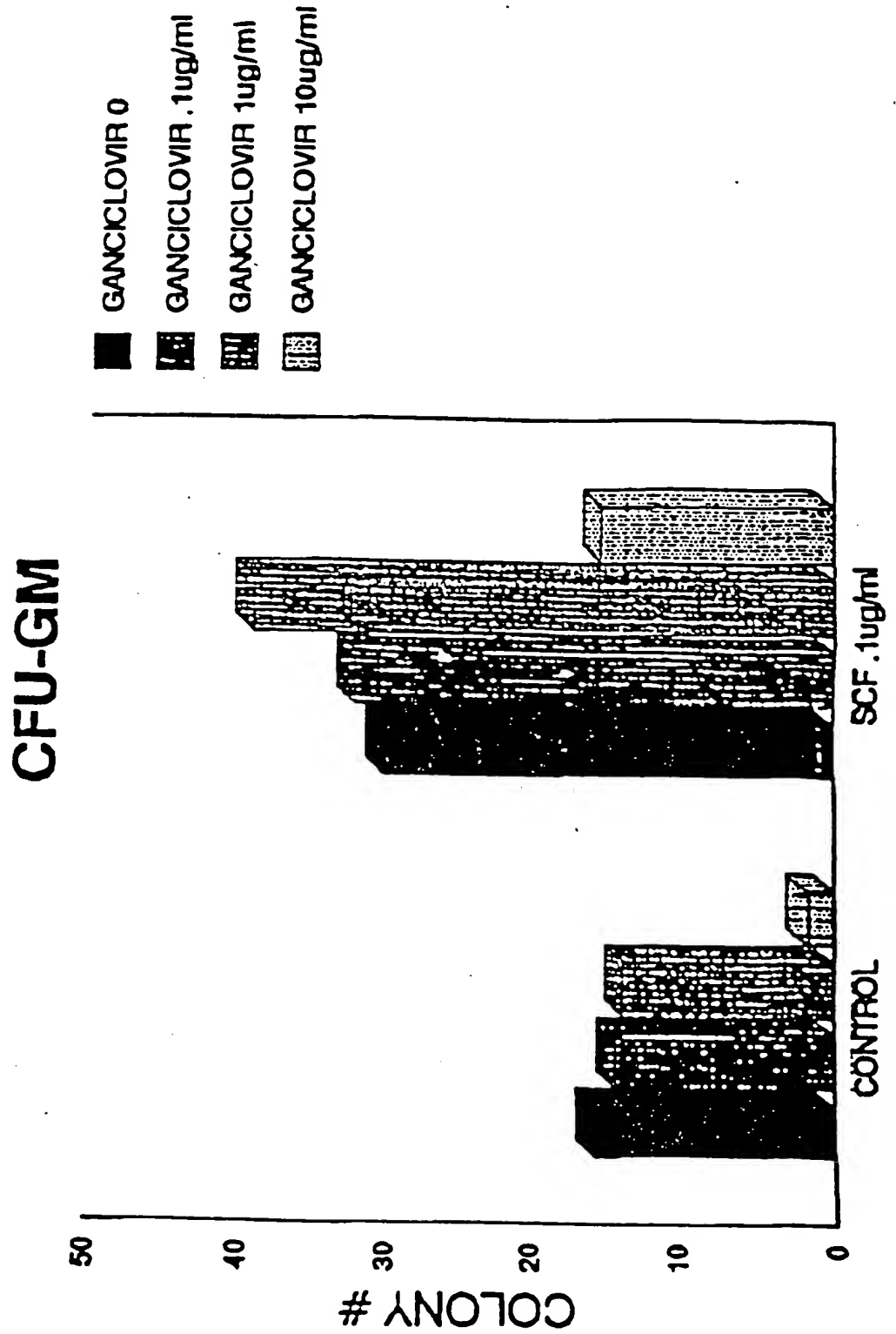


FIG. 66

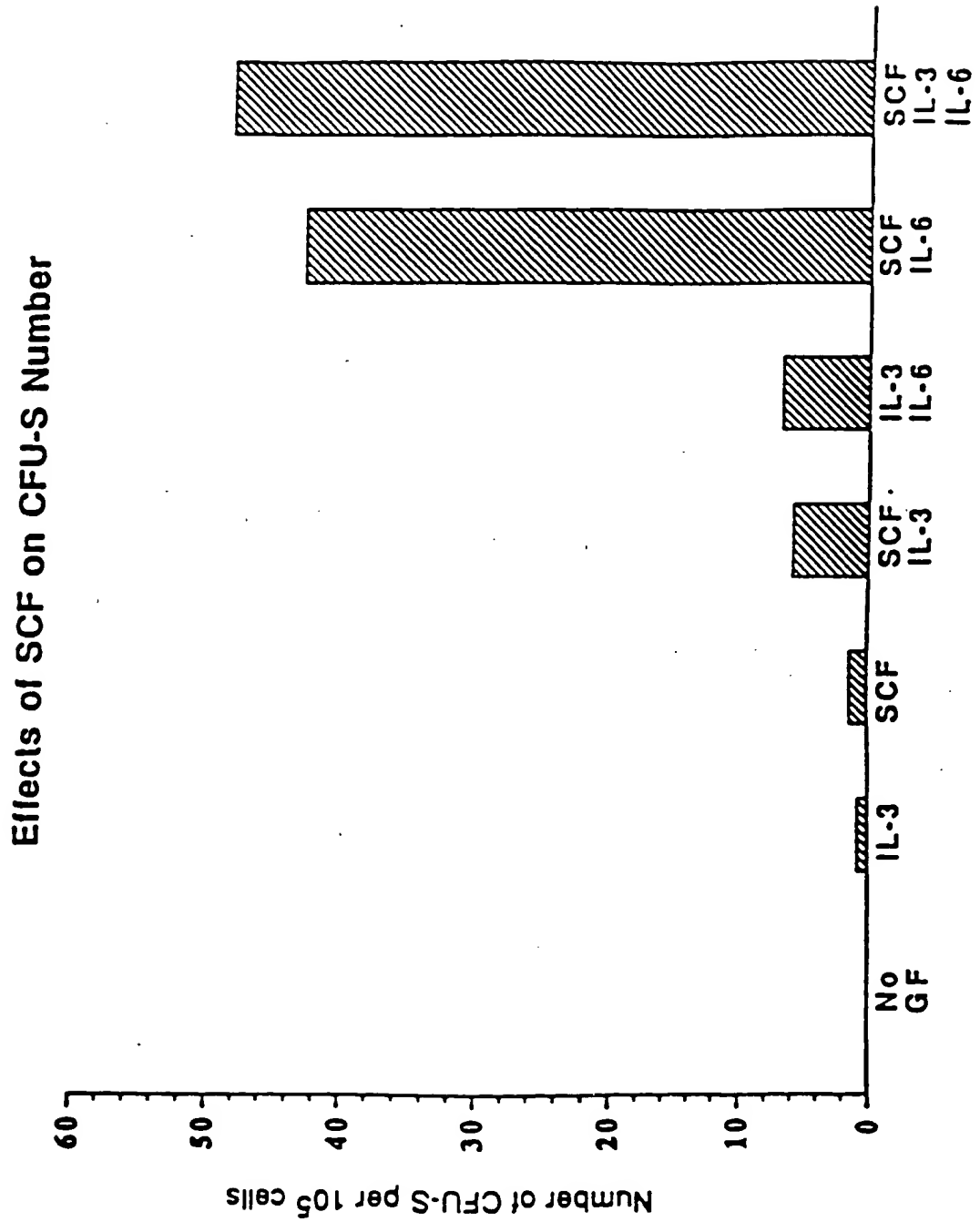


FIG. 67

EFFECTS OF SCF ON SHORT TERM REPOPULATING ABILITY (35 DAYS)

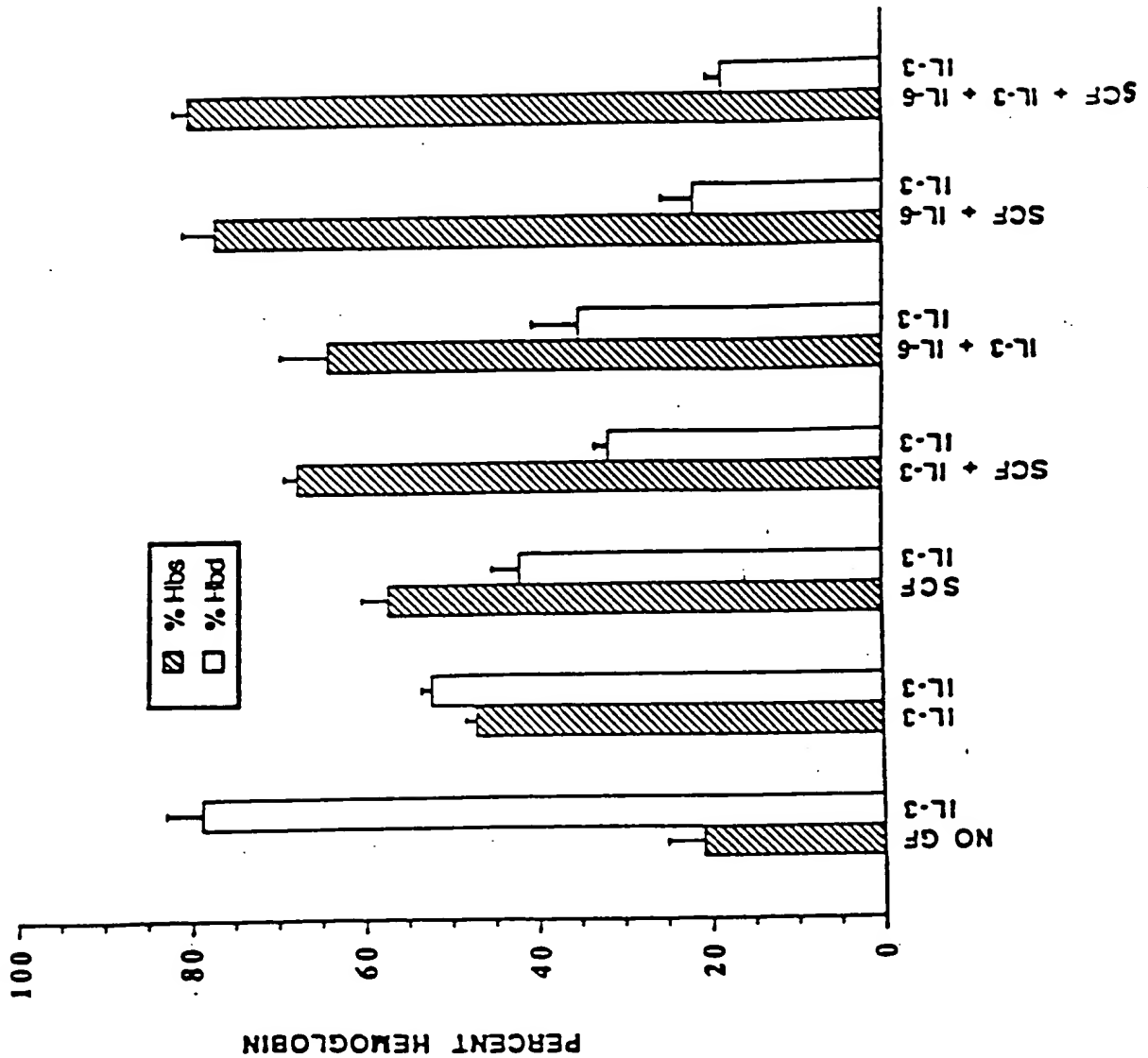


FIG. 68

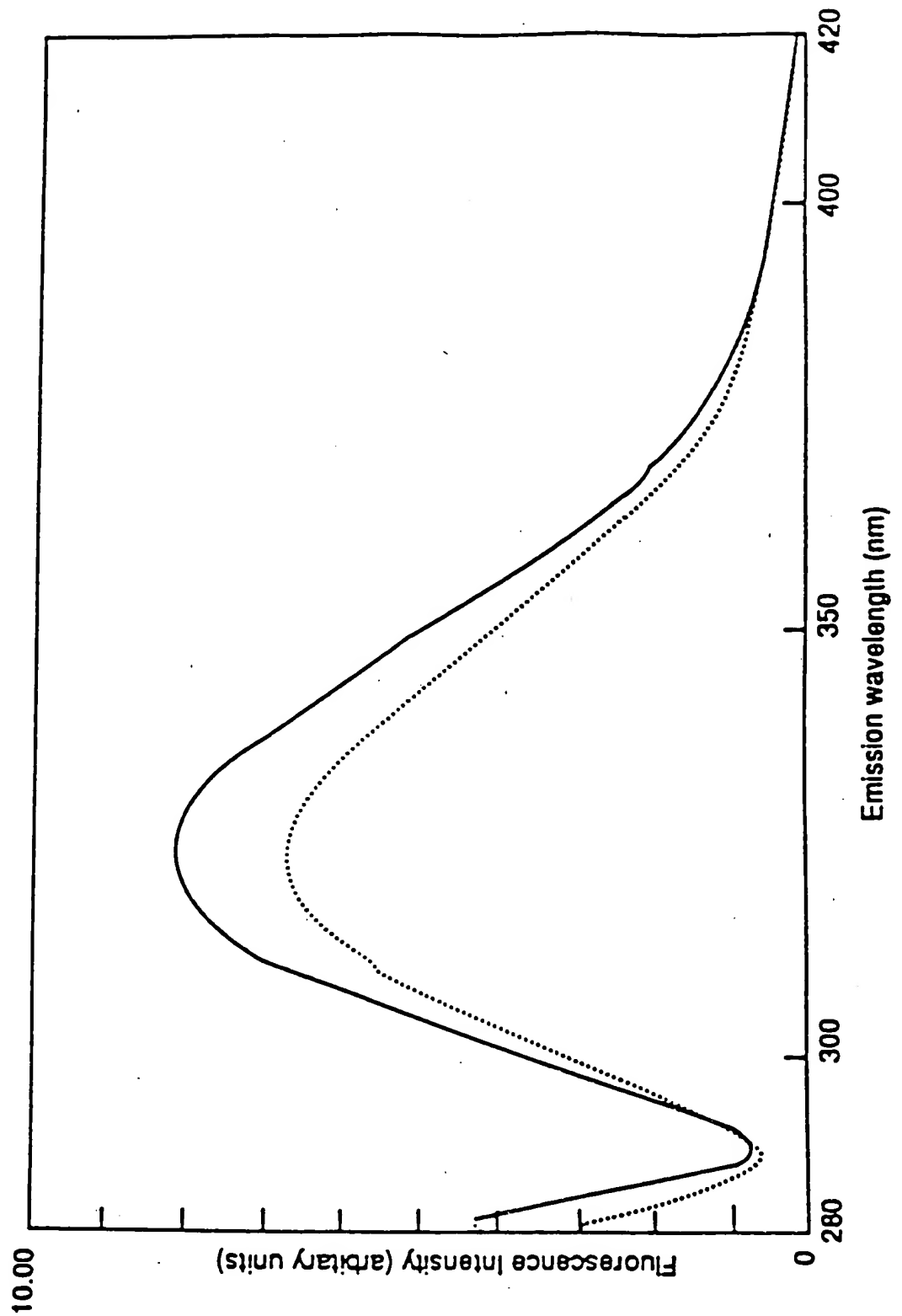


FIG. 69A

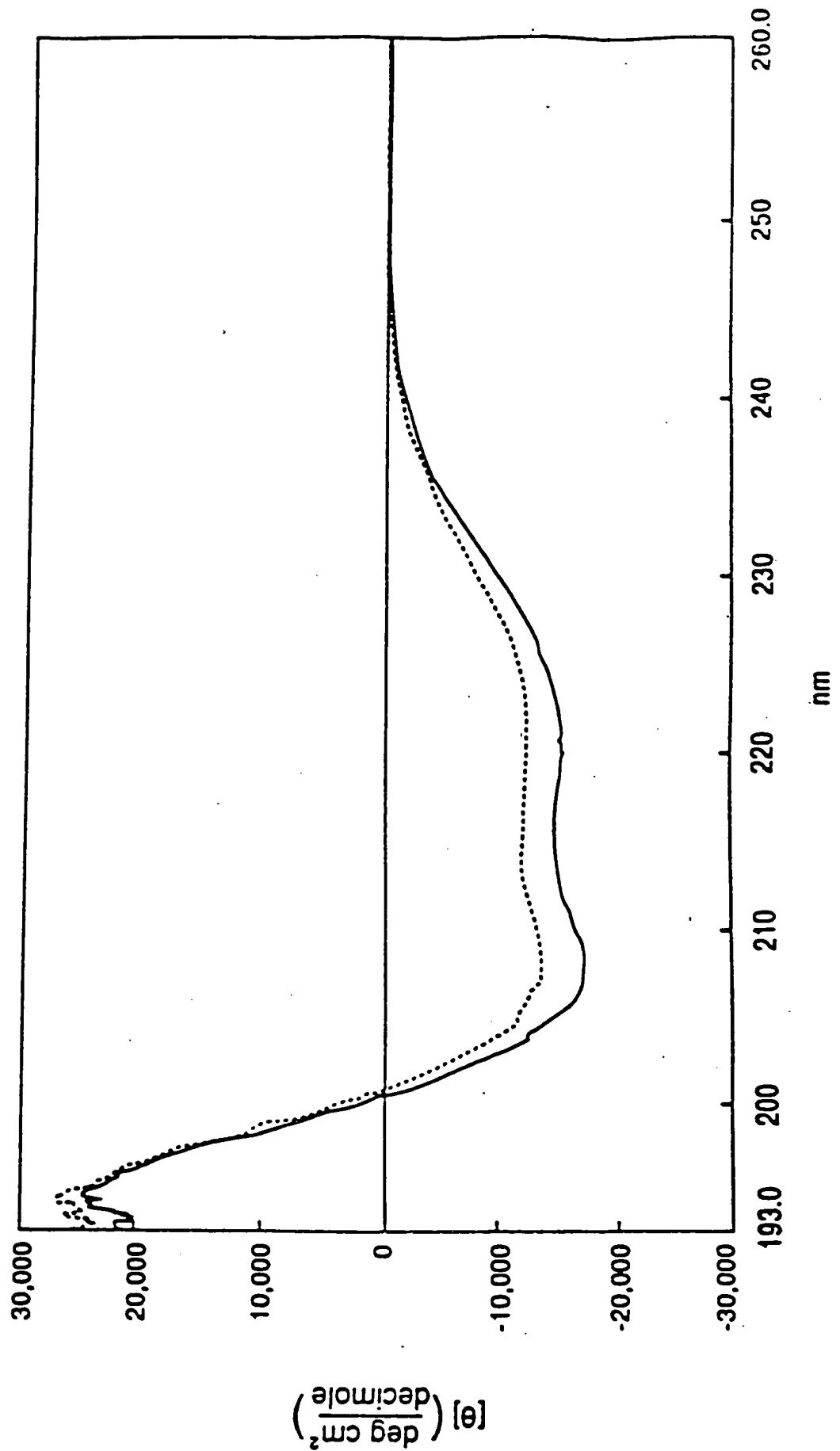


FIG. 69B

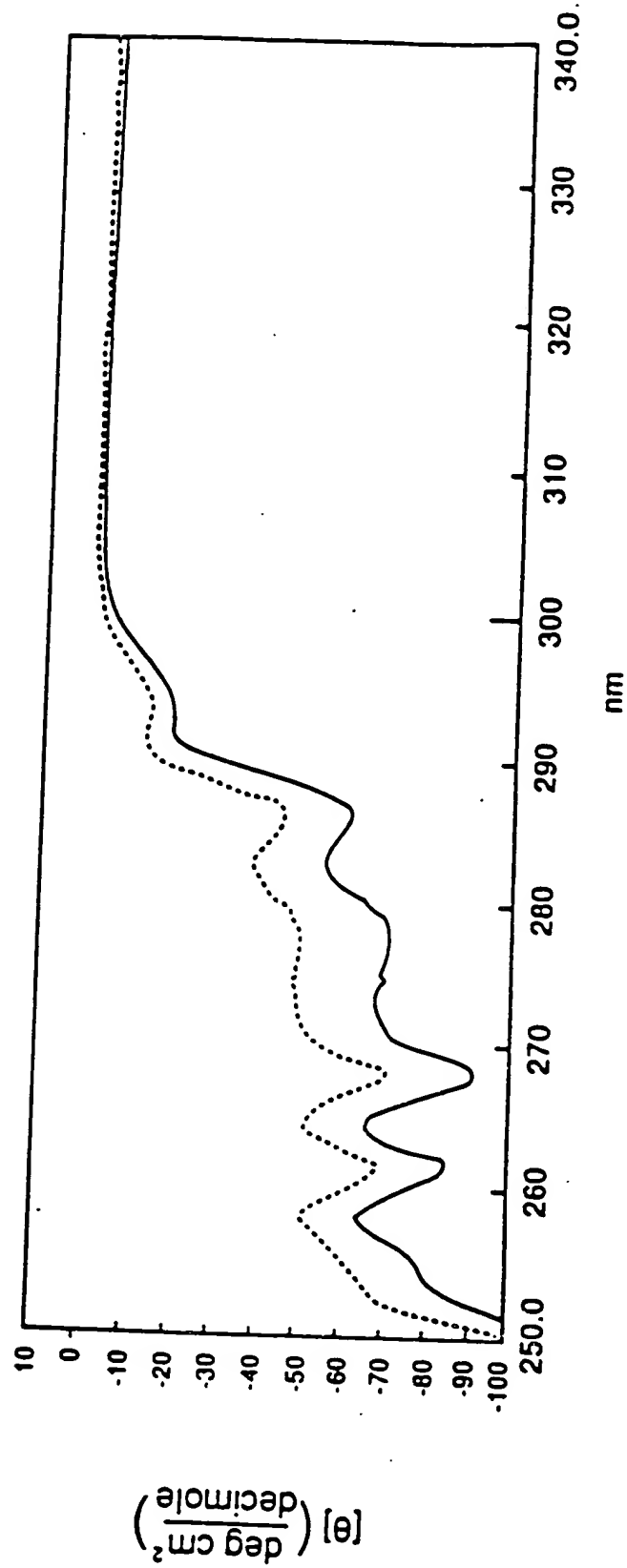


FIG. 70

